

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:24 ; Search time 302 Seconds
(without alignments)
1219.060 Million cell updates/sec

Title: US-10-501-930-1

Perfect score: 2102

Sequence: 1 MRSGGTLFALIGSLMLLLL.....MLQLHMRGILKLPFSKQETA 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2102	100.0	398	1	Q84t1 mus musculus
2	2102	100.0	405	1	Q3t9n4 mouse
3	1936	92.1	398	2	Q6zxc7 rattus norv
4	1922	91.4	362	2	Q8bi43 mus musculus
5	1772	84.3	398	1	P61647 homo sapien
6	1772	84.3	398	1	Q5vzh4 homo sapien
7	1763	83.9	398	1	P61648 pan troglod
8	1597	76.0	398	2	Q5ndg0 bos taurus
9	1183	56.3	398	2	Q6zxc6 gallus gall
10	728	34.6	343	2	Q6kco2 brachydanio
11	727.5	34.6	379	2	Q6kco0 tetraodon n
12	725.5	34.5	378	2	Q5k019 oryza lat
13	719.5	34.2	372	2	Q50j40 fugu rubrip
14	719.5	34.2	379	2	Q6kco1 fugu rubrip
15	715.5	34.0	356	2	Q6kz27 brachydanio
16	710.5	33.8	342	2	P79783 gallus gall
17	703	33.4	356	1	P61642 pan troglod
18	702	33.4	342	2	Q78ei9 rattus sp.
19	701	33.3	356	2	P70554 rattus norv
20	700	33.3	356	1	Q92185 homo sapien
21	700	33.3	356	2	Q6zxc7 rattus norv
22	700	33.3	412	1	P70126 mus musculus
23	699.5	33.3	370	2	Q6kbz8 fugu rubrip
24	697	33.2	355	2	Q8bl76 mus musculus
25	697	33.2	355	2	Q8klc1 mus musculus
26	692	32.9	375	2	Q3trr3 mus musculus
27	691	32.9	355	2	Q8bw10 mus musculus
28	689	32.8	341	2	Q64468 mus musculus
29	688	32.7	376	2	Q8jzq3 mus musculus
30	687.5	32.7	359	2	Q6zxa0 xenopus lae
31	686	32.6	374	2	Q5ndf9 bos taurus

RESULT 1

ID	SIABF_MOUSE	STANDARD;	PHI;	398 AA.
AC	Q8k4t1;			
DT	01-JUN-2004, integrated into UniProtKB/Swiss-Prot.			
DT	01-OCT-2002, sequence version 1.			
DT	07-FEB-2006, entry version 24.			
DE	Alpha-2,8-sialyltransferase 8F (EC 2.4.99.-) (ST8Sia VI).			
GN	Name=St8sia6; Synonyms=St8f;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [mRNA], AND CHARACTERIZATION.			
RX	MEDLINE=22086185; PubMed=1198089; DOI=10.1074/jbc.M112367200;			
RA	Takahama S., Ishida H.K., Inazu T., Ando T., Ishida H., Kiso M.,			
RA	Teuji S., Teujimoto M.;			
RT	"Molecular cloning and expression of a sixth type of alpha 2,8-			
RT	sialyltransferase (ST8Sia VI) that sialylates O-glycans."			
RL	J. Biol. Chem. 277:24030-24038(2002).			
CC	-1- FUNCTION: Prefers O-glycans of N-glycans or glycolipids as acceptor substrates. The mirror image of the NeuAc-			
CC	alpha-2,3(6)-Gal sequence at the nonreducing end of their			
CC	carbohydrate groups.			
CC	-1- PATHWAY: Glycosylation.			
CC	-1- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass			
CC	type II membrane protein (Potential).			
CC	-1- SIMILARITY: Belongs to the glycosyltransferase 29 family.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; AB059554; BAC01265.1; -; mRNA.			
CC	Ensembl; ENSMUSG0000003418; Mus musculus.			
DR	MGI; MGI:2386797; st8sia6.			
DR	GO; GO:0008373; P:sialyltransferase activity; IDA.			
DR	GO; GO:0016051; P:carbohydrate biosynthesis; IDA.			
DR	GO; GO:0009247; P:glycolipid biosynthesis; IDA.			
DR	GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.			
DR	InterPro; IPR01675; Glyco trans 29.			
DR	InterPro; IPR012163; Sialyl transf 29.			
DR	Pham; PFM0777; Glyco transf 29.			
DR	PIRSP; PIRSP005557; Sialyl trans 1.			
KW	Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;			
KW	Signal-anchor; Transferase; Transmembrane.			
CHAIN	1 398 Alpha-2,8-sialyltransferase 8F.			
FT	TOPO_DOM 1 3			
FT	TRANSMEM 4 24			
FT	TOPO_DOM 25 398			
FT	CARBOHYD 66 66			

P61646 pan troglod
Q61aw7 homo sapien
Q6zxc8 rattus norv
Q4suvi tetraodon n
Q6vru1 xenopus lae
Q64687 mus musculus
Q6zxc9 gallus gall
Q6dng6 xenopus tro
O15466 homo sapien
Q3v3b1 mus musculus
Q6kbz9 fugu rubrip
Q50j35 brachydanio
Q4t001 tetraodon n
Q6kcl2 tetraodon n

FT CARBOHYD 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 196 N-linked (GlcNAc...) (Potential).
 FT DISULFID 186 By similarity.
 SQ SEQUENCE 398 AA; 45428 MW; A73A7A2964004917 CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 2102; DB 1; Length 398;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRSQGTFLFALIGSLMLLLMLLMLWCPADAPARSLLMEGSRDTSAAALKTLWSPTTP 60
 Db 1 MRSQGTFLFALIGSLMLLLMLLMLWCPADAPARSLLMEGSRDTSAAALKTLWSPTTP 60
 Qy 61 VPRTRNSTYLDKTTQTEKCDLQYLSNSLNKTRRYSEDDYLTQITNLCRCPPNQA 120
 Db 61 VPRTRNSTYLDKTTQTEKCDLQYLSNSLNKTRRYSEDDYLTQITNLCRCPPNQA 120
 Qy 121 EYDNFRKLASCDAIQDFVVSQNTTPVGTNMSYEVSCKHIPRENIHFMPVPSQPFVD 180
 Db 121 EYDNFRKLASCDAIQDFVVSQNTTPVGTNMSYEVSCKHIPRENIHFMPVPSQPFVD 180
 Qy 181 YPNQCAVNGGILNKLSCGAEIDKSDFPVRCNLPPTITGSASXDVSKNLVTNPSII 240
 Db 181 YPNQCAVNGGILNKLSCGAEIDKSDFPVRCNLPPTITGSASXDVSKNLVTNPSII 240
 Qy 241 TLKYNLKEKKAQFLDSTVGDFAFLLPAPFYPANTGIFPKVYQTLKESQKQKVLFFH 300
 Db 241 TLKYNLKEKKAQFLDSTVGDFAFLLPAPFYPANTGIFPKVYQTLKESQKQKVLFFH 300
 Qy 301 PLYRLHLALFWRTGVTAYRLSTGLMIASVAVELCENVKLYGFWPFKTIETDPLSHYY 360
 Db 301 PLYRLHLALFWRTGVTAYRLSTGLMIASVAVELCENVKLYGFWPFKTIETDPLSHYY 360
 Qy 361 DNMLPKGHFGHMPKEYSQMLQLHMRGILKQFSKCETA 398
 Db 361 DNMLPKGHFGHMPKEYSQMLQLHMRGILKQFSKCETA 398
 RESULT 2
 Q3T9N4 MOUSE PRELIMINARY; PRT; 405 AA.
 AC Q3T9N4;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 5.
 DE Activated spleen cDNA, RIKEN full-length enriched library,
 DE clone:F830206C17 product:Gialyltransferase 8 (alpha-2, 8-
 DE sialyltransferase) F, full insert sequence.
 GN Name=et8sia6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

RA Crowe M.L., Dalla E., Dalrymple
 RA di Bernardo D., Down T., Engstrom
 RA Fletcher C.F., Fukushima T., Furumasa
 RA Georgii-Hemming P., Gingeras T.R.,
 RA Gustincich S., Harbers M., Hayashizaki
 RA Hill D., Huminicki L., Iacono M.,
 RA Jakt M., Kanapin A., Katoh M., Kikawa
 RA Kitano H., Kollias G., Krishnan
 RA Kurochkin I.V., Lareau L.P., Lazarevic
 RA Li S., McWilliam S., Mader M., Marchionni
 RA Matsuda H., Matsuzawa S., Miki H.,
 RA Mottagui-Tabar S., Mulder N., Nakano
 RA Nilsson R., Nishiguchi S., Nishizawa
 RA Okazaki Y., Orlando V., Pang K.C.,
 RA Petrovsky N., Piazza S., Reed J.C.,
 RA Rost B., Ruan Y., Salzberg S.L.,
 RA Schonbach C., Sekiguchi K., Semprini
 RA Shibata Y., Shimada H., Shimada
 RA Sperling S., Stupka E., Sugiyama
 RA Tammoja K., Tan S.L., Tang S.,
 RA Ueda H.R., van Nimwegen E., Verardo
 RA Yamanishi H., Zabarovsky E., Zhu
 RA Grimmond S.M., Teasdale R.D., Li
 RA Wahlestedt C., Mattick J.S., Hume
 RA Fukuda S., Kanamori-Katayama M.,
 RA Iida J., Imamura K., Itoh M., Kato
 RA Kawashina T., Kojima M., Kondo S.,
 RA Nishio T., Okada M., Plessey C.,
 RA Tagami M., Waki K., Watanabe A.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the
 RL Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research
 RG (Genome Network Core Team) and the
 RT "Antisense Transcription in the
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=22354683; PubMed=1246685;
 RA Okazaki Y., Furuno M., Kasukawa
 RA Nikaido I., Osato N., Saito R.,
 RA Yagi K., Tomaru Y., Hasegawa Y.,
 RA Baldarelli R., Hill D.P., Bult C.,
 RA Schriml L.M., Kanapin A., Matsuda
 RA Blake J.A., Bradt D., Brusic V.,
 RA Dalla E., Dragani T.A., Fletcher
 RA Gaasterland T., Gariboldi M., Gissi
 RA Grimmond S., Gustincich S., Hirokawa
 RA Kanai A., Kawai H., Kawasawa Y.,
 RA Konagaya A., Kurochkin I.V., Lee Y.,
 RA Maglott D.R., Maltais L., Marchionni
 RA Nagashima T., Numata K., Okido T.,
 RA Petrovsky N., Pillai R., Pontius
 RA Ravasi T., Reed J.C., Reed D.J.,
 RA Sandelin A., Schneider C., Semprini
 RA Sultana R., Takenaka Y., Taylor
 RA Verardo R., Wagner L., Wahlestedt
 RA Wilming L.G., Wynshaw-Boris A.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimin
 RA Hirozane-Kishikawa T., Konno H.,
 RA Shiraki T., Waki K., Kawai J., Aizawa
 RA Hara A., Hashizume W., Imotani K.,
 RA Miyazaki A., Sakai K., Sasaki D.,
 RA Yasunishi A., Yoshino M., Waters
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).

ome based on functional annotation of

RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1038/35055500;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsumoto H., Aeburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nakaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli P., Suzuki R., Tonita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; AK172400; BAE42986.1; -; mRNA.
 DR MGI; MGI:12386797; st8s1a6.
 DR GO; GO:0008373; F:sialyltransferase activity; IDA.
 DR GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
 DR GO; GO:0009247; P:glycolipid biosynthesis; IDA.
 DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
 DR InterPro; IPR011675; Glyco trans_29.
 DR InterPro; IPR012163; Sialyl trans.
 DR Pfam; PF00777; Glyco trans_29; 1.
 DR PIRSF; PIRSF005557; Sialyl trans; 1.
 KW Glycosyltransferase, Transferase.
 SQ SEQUENCE 405 AA; 46323 MW; 48B7A17BE3443487 CRC64;
 Query Match 92.1%; Score 1936; DB 2; Length 398;
 Query Match 100.0%; Score 2102; DB 2; Length 405;
 Best Local Similarity 100.0%; P-adj. No. 2.5e-156; Indels 0; Gaps 0;
 Matches 398; Conservative 0; Mismatches 0;
 QY 1 MRSGGTIFALIGSLMLLLLRMLPCPADAPARSRLMEGSRDTSGLTSAALKTLWSPPTP 60
 DB 1 MRSGGTIFALIGSLMLLLLRMLPCPADAPARSRLMEGSRDTSGLTSAALKTLWSPPTP 60
 QY 61 VPRTRNSTYLDKTTQITKCKIYOISLSLSNKTTRYSEDDYLOTTINIORCPNROAE 120
 DB 61 VPRTRNSTYLDKTTQITKCKIYOISLSLSNKTTRYSEDDYLOTTINIORCPNROAE 120
 QY 121 EYDNFRKLASCDAIODFVVSQNTVPVTNMSVEVESKKGHIPIRENIFHMFVPSQPFVD 180
 DB 121 EYDNFRKLASCDAIODFVVSQNTVPVTNMSVEVESKKGHIPIRENIFHMFVPSQPFVD 180
 QY 181 YPNQCAVGVNGGILNKLSCGAEIKSDSFVFCNLPITGSASKDVGSKTNLVTNPSII 240
 DB 181 YPNQCAVGVNGGILNKLSCGAEIKSDSFVFCNLPITGSASKDVGSKTNLVTNPSII 240
 QY 241 TLKYNLKEKKAQFLEIDISTYGIIFLLPAPSVRANTGISPKYQTLKESKORQKVLFPFH 300
 DB 241 TLKYNLKEKKAQFLEIDISTYGIIFLLPAPSVRANTGISPKYQTLKESKORQKVLFPFH 300
 QY 301 PVLRLHALFWRTKGVTAFLSTSLMTASVAVELCENVKLYGFWPFPSTIEDTPLSHHY 360
 DB 301 PVLRLHALFWRTKGVTAFLSTSLMTASVAVELCENVKLYGFWPFPSTIEDTPLSHHY 360
 QY 361 DNMLPKHGFHMQPKYSQMLQLFIRGILKLQFSKCTA 398
 DB 361 DNMLPKHGFHMQPKYSQMLQLFIRGILKLQFSKCTA 398
 RESULT 3
 Q6ZXC7 RAT PRELIMINARY; PF0; 398 AA.
 AC Q6ZXC7; 2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Names:SIAT8F;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague Dawley;
 RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
 RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
 RT "The animal sialyltransferases and sialyltransferase-related genes: a
 phylogenetic approach.";
 RL Glycobiology 15:805-817(2005).
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 CC -----
 CC EMBL; AJ699423; CAG27885.1; -; mRNA.
 DR Ensembl; ENSRNOG00000018171; Rat; Mus norvegicus.
 DR GO; GO:0003173; C:integral to GO:gi membrane; IEA.
 DR GO; GO:0008373; F:sialyltransferase activity; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro; IPR001675; Glyco trans_29.
 DR InterPro; IPR012163; Sialyl trans.
 DR Pfam; PF00777; Glyco trans_29; 1.
 DR PIRSF; PIRSF005557; Sialyl trans; 1.
 KW Glycosyltransferase, Transferase.
 SQ SEQUENCE 398 AA; 45271 MW; 8B06509DD781E06 CRC64;
 Query Match 92.1%; Score 1936; DB 2; Length 398;

Best Local Similarity 90.5%; Pred. No. 2.6e-143;
Matches 360; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

QY 1 MRSGGTFLALIGSILMLLLMLWCPADAPARSLMEGSGRETSATKLTWSPPTP 60
DB 1 MRPGGTLFALVGSILMLLLMLWCPADAPARSRMLGEESREETGGTSAALKTLWSPPTP 60
QY 61 VPRTRNSTYLDKTKTQTEKCKLOQLVSLNSKTRRYSEDDYLQITNINQRCFWRQAE 120
DB 61 VPRTRNSTYLDKTPETAERCKGLKYSLSLANKTRRYSEDDYLQITNINQRCFWRQAE 120
QY 121 EYDNFRKALASCCDAQDFVVSQNNTPVGNMSEVESKHIPIRENIHFMPVPSOFFVD 180
DB 121 EYDNFRKALASCCDAQDFVVSQNNTPVGNMSEVESKHIPIRENIHFMPVPSOFFVD 180
QY 181 YPNQCAVGVNGGILNKSCLGAEIDKSDFFVRCNLPLPITGSASQDVGSKTNLTVNPSII 240
DB 181 YPNQCAVGVNGGILNKSCLGAEIDKSDFFVRCNLPLPITGSASQDVGSKTNLTVNPSII 240
QY 241 TLKYQNLKEKKAQFLIEDISTYGBAFLLPAPFSTRANTGIFKVTQTLKESKQKVLFFH 300
DB 241 TLKYQNLKEKKAQFLIEDISAYGDAFLLPAPFSTRANTGIFKVTQTLKESKQKVLFFH 300
QY 301 PRYLRLHALFWRTKGYTAVELSTGLMTASVAVELCENVKLYGFWPFSKTLIEDPLSHYY 360
DB 301 PRYLRLHALFWRTKGYTAVELSTGLMTASVAVELCENVKLYGFWPFSKTLIEDPLSHYY 360
QY 361 DNMLPKHGHOMPEKYSQMLQLHMRGILKQLQFSCETA 398
DB 361 DNMLPKHGHOMPEKYSQMLQLHMRGILKQLQFSCETA 398

RESULT 4
Q8BT43 MOUSE PRELIMINARY; PRT; 362 AA.
AC Q8BT43 MOUSE PRELIMINARY; PRT; 362 AA.
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 13 days embryo lung cDNA, Riken full-length enriched library,
DE clone:D430037E10 product:weakly similar to SIALYLTRANSFERASE 8.
GN Name:st6sia6; Synonyms=Stat8f;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung; STRAIN=C57BL/6J;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung; STRAIN=C57BL/6J;
RC MEDLINE=16141072; PubMed=10349636; DOI=10.1126/science.1112014;
RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impicciato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Keiso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakanishi K., Nakamura S., Norris K.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sander C., Sano S., Sessa L., Sheng Y.,
RA Schonbach C., Sekiguchi K., Sempere C.A., Sessa L., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada S., Silva D., Sincclair B.,
RA Sperling S., Stupka E., Sugura T., Sultana R., Takenaka Y., Taki K.,
RA Tammaja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Veira S., Zimmer A., Hide W., Bult C.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Li E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hum D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Inamori K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawahina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Hibata K., Shiraki T., Suzuki S.,
RA Tagami N., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT "Antisense Transcription in the FANTOM Consortium;
RL Science 309:1564-1566(2005).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=1246685;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogi H., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Shriml L.M., Kanapin A., Matsud H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.S.,
RA Gaasterland T., Gariboldi M., Giesler T., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hiroawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sander C., Schneider C., Sempere C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimin A., Carninci P., Hayashizaki Y.,
RA Hirokawa N., Kondo H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Kawasawa Y., Itoh M., Kagawa I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waters B., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=1121785;
RA Kawai J., Shinagawa A., Shibata K., Kawai T., Hara A., Fukunishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kawai J., Shinagawa A.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T.,

KW Signal-anchor; Transferrase; Transmembrane.
 FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
 FT /Ftrid-PRO_0000149299.
 FT TOPO_DOM 1 3 Cytoplasmic (Potential).
 FT TRANSMEM 4 24 Signal-anchor for type II membrane
 protein (Potential).
 FT TOPO_DOM 25 398 Luminal (Potential).
 FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 196 196 N-linked (GlcNAc...) (Potential).
 FT DISULFID 186 335 By similarity.
 SQ SEQUENCE 398 AA; 44836 MW; 48F58B82E4B69A26 CRC64;
 Query Match 84.3%; Score 1772; DB 1; Length 398;
 Best Local Similarity 82.7%; Pred. No. 2e-130;
 Matches 329; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MRSGGTLFALIGSLMLLLRLMPCADAPARSLMEGSRDTSATSAALKTLWSPPTP 60
 DB 1 MRPGGALLALLALLLLRLMPCADAPGRARILVEESREATHGTTPAALTRLRSPATA 60
 QY 61 VPRTRNSTYLDEKTTQITEKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCPMNRQAE 120
 DB 61 VPRATNSTYLNEKSLQITEKCKNQYIESFSNKTGYSNDYLIQITDIQSCPWKRQAE 120
 QY 121 EYDNFRKLASCDDAIDQDFVVSQNTPVGTNNMSEYVESKHHPIRENIHFMPVSPQFVD 180
 DB 121 EYANFRKLASCDDAIVQNFVVSQNTPVGTNNMSEYVESKEIPIKNIHFMPVSPQFVD 180
 QY 181 YPNQCAVVGNGIILNKSICGAEIDSDVFRCNLPPTTGSASKVDGSKTNLVTNPSII 240
 DB 181 YPNQCAVVGNGIILNKSICGTEIDSDVFRCNLPPTTGDVSKVDGSKTNLVTNPSII 240
 QY 241 TLKYQNLKKAQFLIEDISTYGDALFLLPAFSYRANTGISFKYQYTLKESKMRQKVLFFH 300
 DB 241 TLKYGNLKEKALFLEDIATYGDALFLLPAFSFRANTGTSFKYTYTLESKARQKVLFFH 300
 QY 301 PRLRHALLFWRTKGTAVYRLSTGLMIASVAVELCNVLYGFWPFSKTIETDPLSHHHY 360
 DB 301 PKYLDLALFWRTKGTAVYRLSTGLMITSVAVELCNVLYGFWPFSKTIETDIPVSHHHY 360
 QY 361 DNMLPKGHQHPMPKEYSOMLQHLHMRGILKQFSKCEA 398
 DB 361 DNKLPRKHGHPMPKEYSQILQLHMKGILKQFSKCEVA 398

RESULT 6

QSVZH4 HUMAN PRELIMINARY; PR; 398 AA.
 ID QSVZH4; AC QSVZH4;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Likely ortholog of mouse sialyltransferase 8-VI (Alpha-2, 8-sialyltransferase) (ST8SIA-VI).
 GN Name=RP11-414K1.1; ORFNames=RP11-414K1.1-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Heath P.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Pearce A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AL158164; CAI40658.1; -; Genomic_DNA.
 DR EMBL; AL160289; CAI40658.1; JOINED; Genomic_DNA.
 DR EMBL; AL160289; CAH70722.1; -; Genomic_DNA.
 DR EMBL; AL158164; CAH70722.1; JOINED; Genomic_DNA.
 DR Ensembl; ENSG00000148488; Homo sapiens.
 DR HGNC; HGNC:23317; ST8SIA6.
 DR GO; GO:0030173; C-integral to Golgi membrane; IEA.
 DR GO; GO:0008377; F-sialyltransferase activity; IEA.
 DR GO; GO:0008486; P-protein amino acid glycosylation; IEA.
 DR InterPro; IPR001675; Glyco transferase 29.
 DR InterPro; IPR012163; Sialyl transferase.
 DR Pfam; PF00777; Glyco transferase 29.
 DR PIRSF; PIRSF005557; Sialyl transferase 1.
 KW Glycosyltransferase; Transferrase.
 SQ SEQUENCE 398 AA; 44836 MW; 4F58B82E4B69A26 CRC64;
 Query Match 84.3%; Score 1772; DB 2; Length 398;
 Best Local Similarity 82.7%; Pred. No. 2e-130;
 Matches 329; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MRSGGTLFALIGSLMLLLRLMPCADAPARSLMEGSRDTSATSAALKTLWSPPTP 60
 DB 1 MRPGGALLALLALLLLRLMPCADAPGRARILVEESREATHGTTPAALTRLRSPATA 60
 QY 61 VPRTRNSTYLDEKTTQITEKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCPMNRQAE 120
 DB 61 VPRATNSTYLNEKSLQITEKCKNQYIESFSNKTGYSNDYLIQITDIQSCPWKRQAE 120
 QY 121 EYDNFRKLASCDDAIDQDFVVSQNTPVGTNNMSEYVESKHHPIRENIHFMPVSPQFVD 180
 DB 121 EYANFRKLASCDDAIVQNFVVSQNTPVGTNNMSEYVESKEIPIKNIHFMPVSPQFVD 180
 QY 181 YPNQCAVVGNGIILNKSICGAEIDSDVFRCNLPPTTGSASKVDGSKTNLVTNPSII 240
 DB 181 YPNQCAVVGNGIILNKSICGTEIDSDVFRCNLPPTTGDVSKVDGSKTNLVTNPSII 240
 QY 241 TLKYQNLKKAQFLIEDISTYGDALFLLPAFSYRANTGISFKYQYTLKESKMRQKVLFFH 300
 DB 241 TLKYGNLKEKALFLEDIATYGDALFLLPAFSFRANTGTSFKYTYTLESKARQKVLFFH 300
 QY 301 PRLRHALLFWRTKGTAVYRLSTGLMIASVAVELCNVLYGFWPFSKTIETDPLSHHHY 360
 DB 301 PKYLDLALFWRTKGTAVYRLSTGLMITSVAVELCNVLYGFWPFSKTIETDIPVSHHHY 360
 QY 361 DNMLPKGHQHPMPKEYSOMLQHLHMRGILKQFSKCEA 398
 DB 361 DNKLPRKHGHPMPKEYSQILQLHMKGILKQFSKCEVA 398

RESULT 7

SIA8F PANTR STANDARD; PR; 398 AA.
 ID SIA8F PANTR STANDARD; PR; 398 AA.
 AC P61648;
 DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-JUN-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Alpha-2,8-sialyltransferase 8F (C 2.4.99.-) (ST8SIA VI).
 GN Name=ST8SIA6; Synonyms=SIAT8F;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 NCBI_TaxID=9598;
 [1]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP Harduin-Lepers A., Martinez-Duncanson I., Mollicone R., Delannoy P., Oriol R.;
 RT "Phylogeny of sialyltransferases";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Prefers O-glycans to N-glycans or glycolipids as acceptor substrates. The minimal acceptor substrate is the NeuAc-alpha-2,3(6)-Gal sequence at the nonreducing end of their

CC carbohydrate groups (By similarity).
 CC -1- PATHWAY: Glycosylation.
 CC -1- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass
 CC type II membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 29 family.
 CC
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 CC
 CC EMBL: AJ697663; CAG26901.1; -; mRNA.
 DR InterPro: IPR001675; Glyco trans_29.
 DR InterPro: IPR012163; Sialyl trans.
 DR Pfam: PF00777; Glyco trans_29; 1.
 DR PIRSF: PIRSF005557; Sialyl trans; 1.
 KW Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;
 KW Signal-anchor; Transferase; Transmembrane.
 FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
 FT /Ftrid-PRO_0000149301.
 FT TOPO_DOM 1 3 Cytoplasmic (Potential).
 FT TRANSMEM 4 24 Signal-anchor for type II membrane
 FT protein (Potential).
 FT TOPO_DOM 25 398 Luminal (Potential).
 FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 196 196 N-linked (GlcNAc...) (Potential).
 FT DISULFID 186 335 By similarity.
 FT SEQUENCE 398 AA; 44859 MW; 45794C7A63425554 CRC64;

Query Match 83.9%; Score 1763; DB 1; Length 398;
 Best Local Similarity 82.2%; Pred. No. 1e-129;
 Matches 327; Conservative 31; Mismatches 40; Indels 0; Gaps 0;

QY 1 MRSGGTLFALIGSIMLLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 DB 1 MRPGGALLALLSLLLLLLLLWCPADAPGRARILVEESREATHGTGPAALRLTRSPATA 60
 QY 61 VPRTRNSTYLDKTTQTEKCKDQYSLNSLNTKRYSEDDYLQTTNIQRCFPMNRQAE 120
 DB 61 VPRATNSTYLNKSLHLTECKNKLQVIESFNKTKGYSNDYLQITDIQSCFWRQAE 120
 QY 121 EYDNFRAKLASCDAIQFVVSQNTPVGTNMSYEVEKHHIPIRENIFHMFVVSQPFVD 180
 DB 121 EYANFRAKLASCDAQVNFVVSQNTPVGTNMSYEVEKKEIPIKNIIFHMFVVSQPFVD 180
 QY 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPITGSAKDVGSKTNLVTNPSII 240
 DB 181 YPYNQCAVVGNGGILNKSICGTEIDKSDFFVRCNLPITGSDVSKVGSKTNLVTNPSII 240
 QY 241 TLKYQNLKEKKAQFLEDISTYGFALLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300
 DB 241 TLKYGNLKEKKAQFLEDIATYGAFFLLPAFSFRANTGTISFKVYTLLEESKARQKVLFFH 300
 QY 301 PRLRHALFWRTKGTAVYRLSTGLMTASVAVELCENVKLYGFWPFSKTTEDTPLSHYY 360
 DB 301 PKYLKOLALFWRTKGTAVYRLSTGLMTTSVAVELCKNKLKLYGFWPFSKTTEDIPVSHYY 360
 QY 361 DNMLPKHGHPMPKEYSQMLQLHMRGILKIQFSKCEA 398
 DB 361 DNKLPRGHGHPMPKEYSQILQLHMKGILKIQFSKCEVA 398

RESULT 8

Q5NDG0 BOVIN PRELIMINARY; PRT; 398 AA.
 AC Q5NDG0;
 DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 01-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Alpha-2,8-sialyltransferase (Fragment).
 GN Names: sialT8F;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
 RA Harduin-Leper A., Mollicone R., Delannoy P., Oriol R.;
 RT "The animal sialyltransferases and sialyltransferase-related genes: a
 RT phylogenetic approach.";
 RL Glycobiology 15:805-817 (2005).
 CC
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 CC
 CC EMBL: AJ868431; CA130813.1; -; mRNA.
 DR Ensembl: ENSBTAG00000011366; Bos taurus.
 DR GO: GO:0030173; C: integral to Golgi membrane; IEA.
 DR GO: GO:0008373; F: sialyltransferase activity; IEA.
 DR GO: GO:0006486; P: protein amino acid glycosylation; IEA.
 DR InterPro: IPR001675; Glyco trans_29.
 DR InterPro: IPR012163; Sialyl trans.
 DR Pfam: PF00777; Glyco trans_29; 1.
 DR PIRSF: PIRSF005557; Sialyl trans.
 KW Glycosyltransferase; Transferase.
 FT NON_TER 1
 FT NON_TER 398
 FT SEQUENCE 398 AA; 45033 MW; 549EC59B50CCFD8 CRC64;

Query Match 76.0%; Score 1597; DB 2; Length 398;
 Best Local Similarity 74.6%; Pred. No. 1.e-116;
 Matches 297; Conservative 46; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRSGGTLFALIGSIMLLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 DB 1 MRPGGALLALLSLLLLLLLLWCPADAPGRARILVEESREATHGTGPAALRLTRSPATA 60
 QY 61 VPRTRNSTYLDKTTQTEKCKDQYSLNSLNTKRYSEDDYLQTTNIQRCFPMNRQAE 120
 DB 61 VPRATNSTYLNKSLHLTECKNKLQVIESFNKTKGYSNDYLQITDIQSCFWRQAE 120
 QY 121 EYDNFRAKLASCDAIQFVVSQNTPVGTNMSYEVEKHHIPIRENIFHMFVVSQPFVD 180
 DB 121 EYANFRAKLASCDAQVNFVVSQNTPVGTNMSYEVEKKEIPIKNIIFHMFVVSQPFVD 180
 QY 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPITGSAKDVGSKTNLVTNPSII 240
 DB 181 YPYNQCAVVGNGGILNKSICGTEIDKSDFFVRCNLPITGSDVSKVGSKTNLVTNPSII 240
 QY 241 TLKYQNLKEKKAQFLEDISTYGFALLPAFSYRANTGISFKVYQTLKESKMRQKVLFFH 300
 DB 241 TLKYGNLKEKKAQFLEDIATYGAFFLLPAFSFRANTGTISFKVYTLLEESKARQKVLFFH 300
 QY 301 PRLRHALFWRTKGTAVYRLSTGLMTASVAVELCENVKLYGFWPFSKTTEDTPLSHYY 360
 DB 301 PKYLKOLALFWRTKGTAVYRLSTGLMTTSVAVELCKNKLKLYGFWPFSKTTEDIPVSHYY 360
 QY 361 DNMLPKHGHPMPKEYSQMLQLHMRGILKIQFSKCEA 398
 DB 361 DNKLPRGHGHPMPKEYSQILQLHMKGILKIQFSKCEA 398

RESULT 9

Q6ZXC6 CHICK PRELIMINARY; PRT; 398 AA.
 AC Q6ZXC6;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Names: sialT8F;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; C


```
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Leperc A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
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CC -----
DR EMBL; AJ699424; CAG27886.1; -, mRNA.
DR GO; GO:0030173; C: integral to Golgi membrane; IEA.
DR GO; GO:000373; F: sialyltransferase activity; IEA.
DR GO; GO:0006486; P: protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans.29.
DR InterPro; IPR012163; Sialyl trans.
DR Pfam; PF00777; Glyco trans.29; 1.
DR PIRSF; PIRSF005557; Sialyl trans; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 398 AA; 44877 MW; 7D334FF316460667 CRC64;

Query Match 56.3%; Score 1183; DB 2; Length 398;
Best Local Similarity 60.7%; Pred. No. 3.5e-84;
Matches 224; Conservative 49; Mismatches 90; Indels 6; Gaps 2;

QY 35 LLMGSRD---TSGTSAALKTLWSPPTVPTRNSTVLDK---TQITEKCKDLOVSL 88
DB 29 LLARGWEEAEVATVTKVVALRSPLTSLPTQENRTANKDGIYQELDTCKKAIQDNI 88

QY 89 NSLSNKTRRYSEDDYLOITINIQRCPNRQAEYDNFRAKLASCCDAIQDFVWSQNTPTV 148
DB 89 LSSSFKKRYEDYVYHVKLQNCQTVWRPEESAKFSELSACNVAHNPFIASQNTPL 148

QY 149 GTNMSYEVESKXKPIPIENIFHMPFVSQPFVDYPNQCAVVGNGIILKSLCGAEIDKSD 208
DB 149 GSNMSYEVDSKKTILITIEDIFMLPVSPSLVSPFQCAVVGNGIILKSLCGAEIDRSD 208

QY 209 VFVRCNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFL 268
DB 209 VFVRCNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFL 268

QY 269 PAFSFRNTATSPKYYHTLQEFKATQRAIPFPHTYLNLAQFWRTKGKAYRLSSGFMIT 328
DB 269 PAFSFRNTATSPKYYHTLQEFKATQRAIPFPHTYLNLAQFWRTKGKAYRLSSGFMIT 328

QY 329 SVAVELCENKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGIL 388
DB 329 SAAVELCENKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGIL 388

QY 389 KLPQSKCET 397
DB 389 KLPQSKCES 397

RESULT 10
Q6KC02_BRARE PRELIMINARY; PRT; 343 AA.
AC Q6KC02;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name=siat 8E;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=9555;
RN [1]
RP NUCLEOTIDE SEQUENCE.

QY 35 LLMGSRD---TSGTSAALKTLWSPPTVPTRNSTVLDK---TQITEKCKDLOVSL 88
DB 29 LLARGWEEAEVATVTKVVALRSPLTSLPTQENRTANKDGIYQELDTCKKAIQDNI 88

QY 89 NSLSNKTRRYSEDDYLOITINIQRCPNRQAEYDNFRAKLASCCDAIQDFVWSQNTPTV 148
DB 89 LSSSFKKRYEDYVYHVKLQNCQTVWRPEESAKFSELSACNVAHNPFIASQNTPL 148

QY 149 GTNMSYEVESKXKPIPIENIFHMPFVSQPFVDYPNQCAVVGNGIILKSLCGAEIDKSD 208
DB 149 GSNMSYEVDSKKTILITIEDIFMLPVSPSLVSPFQCAVVGNGIILKSLCGAEIDRSD 208

QY 209 VFVRCNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFL 268
DB 209 VFVRCNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFL 268

QY 269 PAFSFRNTATSPKYYHTLQEFKATQRAIPFPHTYLNLAQFWRTKGKAYRLSSGFMIT 328
DB 269 PAFSFRNTATSPKYYHTLQEFKATQRAIPFPHTYLNLAQFWRTKGKAYRLSSGFMIT 328

QY 329 SVAVELCENKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGIL 388
DB 329 SAAVELCENKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGIL 388

QY 389 KLPQSKCET 397
DB 389 KLPQSKCES 397

RESULT 10
Q6KC02_BRARE PRELIMINARY; PRT; 343 AA.
AC Q6KC02;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name=siat 8E;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=9555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

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RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Leperc A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ715546; CAG29385.1; -, mRNA.
DR GO; GO:0030173; C: integral to Golgi membrane; IEA.
DR GO; GO:000373; F: sialyltransferase activity; IEA.
DR GO; GO:0006486; P: protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans.29.
DR InterPro; IPR00777; Glyco trans.29.
KW Glycosyltransferase; Transferase.
FT NON_TER 1 343
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 39768 MW; 2B686D818AC9136 CRC64;

Query Match 34.6%; Score 728; DB 2; Length 343;
Best Local Similarity 44.2%; Pred. No. 1.5e-48;
Matches 134; Conservative 56; Mismatches 113; Indels 0; Gaps 0;

QY 93 NKTRRYSEDDYLOITINIQRCPNRQAEYDNFRAKLASCCDAIQDFVWSQNTPTVGTNM 152
DB 40 NYIKRVKTSLEFRWRNLQVCKVQNKKEETDNFMSLSRCCNAPSFLLTKRNTPSGPKL 99

QY 153 SYEVESKXKPIPIENIFHMPFVSQPFVDYPNQCAVVGNGIILKSLCGAEIDKSDVFR 212
DB 100 RYEVDTSGIILHISPEIFKMPDDPFSKSFQKCAVVGNGIILKSLCGAEIDKSDVFR 159

QY 213 CNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFLPAPS 272
DB 160 CNLPPTGASKDVGSKTNLVNPSIITLKYQNLKKAQFLEIDISTYGDALFLPAPS 219

QY 273 YRANTGISFKVYQTLKESKMRQKLPFPYRLHRLALFWRTKGVTAYRLSTGLMIASVAV 332
DB 220 NTRNTDVSFVKYMLDDFESSRGFFPHQYLLNVQRFVAVQVRAKRLSSGLMLVTAAM 279

QY 333 ELCEVNLKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGILKIQF 392
DB 280 ELCEVNLKLYGFWPFPSKTIETDPLSHHYDNLMPKHGFHOMPKYSQMLQLHMRGILKIQF 339

QY 393 SKC 395
DB 340 GPC 342

RESULT 11
Q6KC00_TETNG PRELIMINARY; PRT; 379 AA.
AC Q6KC00;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name=siat 8E;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Ecomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodontidae.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Leperc A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
```


Query Match	34.2%	Score 719.5	DB 2	Length 379
Best Local Similarity	41.9%	Pre. No. 7.9e-48		
Matches 132	Conservative	Mismatches 61	Indels 1	Gaps 1
Qy	81	CKDLQVSLNSLNSKTRRYSDDY	QTTNTLQRCPPNWRQAEYDNFRAKLASCDDAIDQFV	140
Db	65	CRELRQEMDVKVL-T-MKTSDI	ERWRNLQICWEQNKETSFPKMSLRCCNAPSLF	123
Qy	141	VSQNNTPVQTMNYSYEVESKKHIE	RENIFHMFVPVSQFVDYPYNQCAVGVNGGILNKSCL	200
Db	124	TTKENTPAGTKLRYEVDVTSGLIE	TAEVFQMFDPDMPSYKQPKCAVGVNGGIKNSKC	183
Qy	201	GAEDIKSDFFRCNLPLPITGSAS	DVGSKTNLTVTVNPSIITLKYNLKEKKAQFLEIDIST	260
Db	184	GKEIDSADFRCNIPPIISIKYS	DVGTKTDLVSINPSIITERFQKLEKRRRPFEYLN	243
Qy	261	YGDAFLLPAPFSYRANTGIFSKY	QTLKESKMRQKVLFFHPYLRHLALFWRTKGVTAJR	320
Db	244	YENSSAVLPAPYTRNTDVSFRV	LYMLDDTDSQGVFFHPHPQYLLNVQRFWAVGVRAKR	303
Qy	321	LSTGLMTASVAVELCENVKLYGE	PPFSKTIETDPLSHHYDNNMLPKRGFHPQMPKEYSQML	380
Db	304	LSSGLMLVTAALENCEVEHLYGE	YAFPMNPSGFIITHYHYDNNVKPRPGGFHAMPHIEIFNFI	363
Qy	381	QLHWRGILKIQFSKC		395
Db	364	HMETRGIVNVHTGQC		378

RESULT 15	Q6KBZ7_BRARE	PRELIMINARY;	PF	356 AA.
ID	Q6KBZ7_BRARE	integrated into UniProtKB/TrEMBL.		
AC	Q6KBZ7;	05-JUL-2004, sequence version 1		
DT	05-JUL-2004,	entry version 10.		
DT	07-FEB-2006,			
DT	Alpha-2,8-sialyltransferase ST8S	a VI (EC 2.4.99.8) (Fragment).		
DE	Name=sialt 8F;			
GN	Brachydanio rerio (zebrafish) (Danio rerio).			
OS	Chordata; Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
OX	[1]			
RN	NUCLEOTIDE SEQUENCE.			
RP	PubMed=15843597; DOI=10.1093/glycob/cwi063;			
RX	Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;			
RA	The "animal sialyltransferases and sialyltransferase-related genes: a			
RA	phylogenetic approach."			
RT	Glycobiology 15:805-817(2005).			
RL				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	-----			
CC	ENBL; AJ715551; CAG29390.1; -; rRNA.			
DR	Ensembl; ENSDARG0000021195; Danio rerio.			
DR	GO; GO:0030173; C:integral to Golgi membrane; IEA.			
DR	GO; GO:0003828; F:alpha-N-acetylneuraminic acid glycosylation; IEA.			
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.			
DR	InterPro; IPR001675; Glyco trans_29.			
DR	Pfam; PF00777; Glyco_transf_29; -			
KW	Glycosyltransferase; transferase			
FT	1			
FT	NON TER			
FT	356			
FT	SEQUENCE			
FT	356 AA; 40331 MW; 1			
FT	2228C77673558A CRC64;			
FT				
FT	Query Match			
FT	34.08; Score 715.5; DB 2; Length 356;			
FT	Best Local Similarity			
FT	40.28; Prob. No. 1.5e-47;			
FT	Matches 138; Conservative			
FT	Indels 25; Gaps			
FT				
Qy	57 PTPVPVPRTRNSVLDEKTTQITE			
Qy	CKDLOYSLNSLNKTRRYSEDDYLQTITNRCQPN 116			
Db	38 PASRIPOKSN-----TOSCK			
Db	CKDSVIGKALGN-----YNS			
Db	-----WK 73			

A;Residues: 16-356 <R2>
A;Cross-references: UNIPARC:UIP00001976C8; GB:D26360; NID:g536879; PIDN:BAA05391.1; PIDD:
C;Genetics:
A;Gene: GDB:SIA78
A;Cross-references: GDB:370916; OMIM:601123
A;Map position: 12p12.1-12p11.2
C;Superfamily: sialyltransferase
C;Keywords: Glycosyltransferase, transmembrane protein

Query Match 33.3%; Score 700; DB 2; Length 356;
Best Local Similarity 43.6%; Pred. No. 2.3e+48;
Matches 130; Conservative 59; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQTITNIQRCPWNRQAEDINFRAKLASCDAIQDFVVSQNTPVGVTNNSEYVES 158
:: ::
Db 53 NEKEIVGVGLG-QGTAWERNQTAPAFRRKQMDECCDPAHLFAMTKMSPMGSKWVDGEF 111
:
Qy 159 KKHPIRENIHFMPVPVSOPFDYPNQCAVVNGGIINKSLCGAEIKDSDFVFRCNLPP1 218
:
Db 112 LYSTINDSTVLSLPFOATPFQQPLKKCAVNVGGILKSGCGROIDEANFMVCNLPLL 170
:
Qy 219 TGSASKDVGSKTNLTVNPISITLKYNQLKEKAQFLIEDISTYGDAFLLLPFPASYRANTG 278
:
Db 171 SSETKDVGSKSQLVTAAPSIIIFRFONLLWSRKTFVDNMKIYNHSIYYMPAFSMKTCTE 230
:
Qy 279 ISFKYOTLKESKMOKVLFFHRYLRHALFWRTKVGYTAYRLSTGLMIASVAVELCEV 338
:
Db 231 PSLEVVYTLDVGANGQTVLFANEWFERSIGCFWKSRGIIHAKRILTGLFLVASALGLCEEV 290
:
Qy 339 KLYGFWPFSKITETPLSHHYVLMKPKGHPOMPKEYSOMLOLHMREGILKLQFSKCE 396
:
Db 291 AIYGFWPFSVNHBQPISHHTYTRVLPFGFHAMPPEFLQLTYLHKLGALKRMQLDPCE 348
: :

RESULT 4
JC5600
alpha-N-acetylneuraminat alpha-2,8-sialyltransferase (EC 2.4.99.8) - human
C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Oct-2004
C;Accession: JC5600
R;Kim, Y.J.; Kim, K.S.; Do, S.; Kim, C.H.; Kim, S.K.; Lee, Y.C.
Biochem Biophys Res Commun. 235, 327-330, 1997
A>Title: Molecular cloning and expression of human alpha-2,8-sialyltransferase (hsrStsia
A;Reference number: JC5600; PMID:9732494; PMD:9199191
A;Accession: JC5600
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-376 <KIM>
A;Cross-references: UNIPROT:O15466; UNIPARC:UIP0000135974; GB:U91641; NID:g2353693; PIDN:
A;Comment: This enzyme catalyzes the formation of an alpha-2,8-sialyl linkage by transfer
or the production of disialyl or trisialyl structures containing alpha-2,8-sialyl linkage
C;Superfamily: sialyltransferase
C;Keywords: Glycosyltransferase

Query Match 32.2%; Score 677; DB 2; Length 376;
Best Local Similarity 43.9%; Pred. No. 1.7e+46;
Matches 126; Conservative 53; Mismatches 108; Indels 0; Gaps 0;

Qy 109 NIQCPCPNRAEEVDNFRAKLSCDAIQDFVVSQNTPVGVTNNSEYVESKKHIPIREN1 168
:
Db 87 SLWCCKWANNTSEANQKFXTLSFCNCNAFLFTTQKNPTLGTKKYEVDTSGVIHINGEI 146
:
Qy 169 FHMFVPVSOPFDYPNQCAVVNGGIINKSLCGAEIKDSDFVFRCNLPPITGSASKOVYS 228
: ~~~~~~
Db 147 FRMEPKMPIYRSQPKCAVNVGGILNKNSCRGREINSADFVFRCNLPPISEKVTMDVGV 206
: ~~~~~~
Qy 229 KTNLTNVNPSIITLKYNQLKEKAQFLIEDISTYGDAFLLLPFPASYRANTGISFKVYQTLK 288
: ~~~~~~
Db 207 KTDVVTVNPSIITERFHHKLEKWRFPRFYRVLYVENAVSVLLPFAFYNTNTDIISRISKYILD 266
: ~~~~~~
Qy 289 ESKMKVKVLPFHRYLRHALFWRTKVGYTAYRLSTGLMIASVAVELCEVNLKYGFWPFSK 348
: ~~~~~~

[illegible]



[illegible]

```

RESULT 11
A46727
sialyltransferase (EC 2.4.99.-), brain, precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Oct-2004
C/Accession: A46727
R/Livingston, B.D.; Paulson, J.C.
J. Biol. Chem. 269, 11504-11507, 1993
A/Title: Polymerase chain reaction cloning of a developmentally regulated member of the
A/Reference number: A46727; MUID:93280099; PMID:7685014
A/Accession: A46727
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-375 <LIV>
A/Cross-references: UNIPROT:Q0977; UNIPARC:UPI0000135971; GB:IL13445; NID:9310229; PIDN:
C/Superfamily: sialyltransferase
C/Keywords: glycosyltransferase

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Query Match	19.2%	Score	403.5	DB 2	Length	375			
Best Local Similarity	28.6%	Pred. No.	1.4e-24						
Matches	99	Conservative	62	Mismatches	142	Indels	43	Gaps	7
Qy	84	LOYSLSLSNKTTRYSEDDYLIQITNIQRCP-----WNRQAEYD	123						
Db	41	IRSAVNSLSHKSNR-----AEVINGSLSFAVADRSNESLKHSIQPASSKWRNRNQTLSL	94						
Qy	124	NFRAKLASCCDAIQDFVVSQNNPTVGTNMSYEVSCKHIPIRENIHFMPVPSQPFVDYPY	183						
Db	95	RIRQIILFLDREKDISVLKTLFPGDIHVIYFDRDSTMVSNQLYELLPTSLKNGHF	154						
Qy	184	NQCAVNGNGILNKLSCGAIEKSDSFVRCNLPPIITGSASKDVGSKTNLVTVNPSIITLK	243						
Db	155	QTCAlVGNISGVLLNSGCGQEIETHSFVIRCNLAPVQEYA-RDVGLKTDLVTMNPSVIQRA	213						
Qy	244	QYNI-----KEKKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVYQTLKESKMRQKVL	298						
Db	214	FEDLVNATWREKLQRLHGLN---GSLIMWIPAFMARCGKERVEVWNAIILKHVNVRATY	270						
Qy	299	FHPYLRHLALFWRTKGTVAURLSTGLMASVAVELCENVKLYIGFWPPSKTIEDTPLSHH	358						
Db	271	PSLELLHARVGYLWNTKVKHIIKRPITGLMYLATRFNCQIYLYGFWEFPDLDQNFVKYH	330						
Qy	359	YYDNMLPKHGF-----HOMPKYSQMLQLHMRGILKLOFSCBETA	398						
Db	331	YYDSI--KYGYTSAOSPHTMPLFEPKALKSLSHEOGALKLTVGCDDGA	374						

RESULT 12

148686 N-glycan alpha 2,8-sialyltransferase - mouse.

C:Species: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004

C/Accession: I48686

R:Kojima, N.; Yoshida, Y.; Kurosawa, N.; Lee, Y.C.; Teuji, S.

FEBS Lett. 360, 1-4, 1995

A:Title: Enzymatic activity of a developmentally regulated member of the sialyltransferase

A,Reference number: I48686; MUID:95180406; PMID:7875291
A,Accession: I48686
A,Status: preliminary; translated from GB/EMBL/DBJ
A,Molecule type: mRNA
A,Residues: 1-375 <RES>
A,Cross-references: UNIPROT:Q35696; SWISSPROT:Q35696; SWISS-PROT:Q35696; SWISS-PROT:Q35696; SWISS-PROT:Q35696
C,Superfamily: siatyltransferase

Query Match	18.8%	Score 395.5;	DB 2;	Length 375;
Best Local Similarity	29.2%	Prod. NO. 6e-24;		
Matches 100;	Conservative 63;	Mismatches 144;	Indels 35;	Gaps 8

```

Qy 84 LQVSLNSLSNKTTRYSS-----EDDYLOQTITNIQ--RCPNWQAQAEYVDNFA 127
Db 41 IRSAVNSLSHKSNAEAVVINGSPPAVADRSNESLK--HNIQPASSKWRHNQOTLSLRK 98
Qy 128 KLASCCDAIQFVVVSQNNTPVGNMSYEVSRSKXHIPIREMIFHFPVSPQFVDYPIYNQCA 187
Db 99 QILKFLDAEKDISVLKGTLPKGLIHIFDRDSTMNVSQLYELLPRTPSLPNKXHFOTCA 158
Qy 188 VVNGGILNKSLCGAEIDKSDFFRCMLPITGSASKDVSGSKTNLVTVPNSIITLKYNQL 247
Db 159 IVNGSGVLLNSGGCGQEIDTSHFIRCNRA5VQEYA-RDVGLKTLDTVMNPSVIORAFEDL 217
Qy 248 -----KEKKAQFLEDISTYGDALLLPAFSYRANTGISFKYQYOTLKESQMRQVLFPHPR 302
Db 218 VNATWREKLLQRLHGLN--GSLWIPAFWARGGKERVWVNALILKHHVNVRTAYPSLR 274
Qy 303 YLRHLALFWRTKGTAYTARLSTGLMIASVAVELCENVKLXGFWPSPSKTIEDTPLSHHYVDN 362
Db 275 LLHAVRGYWLTKVHKHCRPTTGLMYTLATFCNQIYLYGFWPFPDQNPQNVKHYHYDS 334
Qy 363 MLPKHGF-----HOMPKYSOQLQHMGRILKILQFSKCETA 398
Db 335 L--KYGVTSOASPHTMPLFPAKLSLHOCAGLKTVGOCDBA 374

```

RESULT 13
B54898
STX protein - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 05-Oct-2004
C/Accession: B54898
R:Kitagawa, H.; Paulson, J.C.
J. Biol. Chem. 269, 17872-17878, 1994
A/Title: Differential expression of five sialyltransferase genes in human t
A/Reference number: A54898; MUID:94239495; PMID:8027041
A/Accession: B54898
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-222 <KIT>
A/Cross-references: UNIPROT:Q92186; UNIPARC:UPI0000149059; GB:L29556; NID:9
C/Superfamily: sialyltransferase

	Query Match	16.8%	Score 352.5;	DB 2;	Length 222;
	Best Local Similarity	35.2%;	Prod. No. 8e-21;		
	Matches	80;	Conservative 42;	Mismatches 88;	Indels 17; Gaps 5;
Qy	183	YNOCVVNGGIIKSLKCGAEI	KSFVFRCNLPPIITGASKDVGSKTNLVTNPSIITL	242	
Db		:			
Db	1	FQCAIVGSGVLLNGYGOEI	HAHGFVRCNLAPQVEYA-RDVLKTDLTVTNPSVIQR	59	
Qy	243	KYQNL-----KEKKAQFLEDIS	YGDAPFLLLPAPSYRANTGISFKYQTLKESMKQKVL	297	
Db		:			
Db	60	AFEDLVNATWREKLLQRLHSLN	--GSIIWIPAFMARGGKERVEYNELIKHGVNVRTA	116	
Qy	298	FHPHYRLHLAFLWRKGTVAY	TLSTGLMIASVAVELCENVKLYGFWPSPKTIETPLSH	357	
Db	117	YPSRLLLHVRGWLTKNKHIK	PTTGLLMYTLATREFCKIYLYGFWPFPDQNPVKY	176	
Qy	358	HYTDNMLPKHGF-----HOMP	EYSQMLQLHWRGILKIQFSKETA	398	
Db	177	HYTDSL--KYGYTSQSASPTMP	EFKALKSLHQGALKLTVGCGDA	221	

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:10 ; Search time 197 Seconds
(without alignments)
923.716 Million cell updates/sec

Title: US-10-501-930-1

Perfect score: 2102

Sequence: 1 MRSGLTLPALIGSLMLLLL.....MLQLHMRGILKIQSKCETA 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2102	100.0	398	7	ADC73011 Murine ST
2	1768	84.1	398	7	ADC73013 Human ST8
3	1180	56.1	247	4	AAG66954 Human sia
4	1180	56.1	247	8	ADV69201 Human cel
5	701	33.3	359	7	AD56214 Rat Prote
6	700	33.3	341	2	AAR83226 Human alp
7	700	33.3	356	2	AAR63225 Human alp
8	697	33.2	356	4	AAB86207 Human GD3
9	477.5	22.7	380	7	ADD48076 Human Prote
10	474	22.5	380	7	ADD48074 Rat Prote
11	470	22.4	339	2	AAW05301 Extracell
12	470	22.4	380	5	ABB57203 Mouse isc
13	470	22.4	381	2	AAW05300 Sia alpha
14	419.5	20.0	359	2	AAR97868 Hamster p
15	418.5	19.9	359	7	AD660174 Rat Prote
16	416.5	19.8	359	7	AD660176 Human Pro
17	416.5	19.8	359	7	ADD48964 Human Pro
18	416.5	19.8	359	9	ADD48172 Human Pro
19	416.5	19.8	359	9	ADX57715 Rheumatoid
20	416.5	19.8	359	9	ADY15754 PRO poly
21	403.5	19.2	375	2	AAR48342 Rat sialy
22	399.5	19.0	353	7	ADD48962 Rat Prote
23	399.5	19.0	353	7	ADD48170 Rat Prote

24	399.5	19.0	375	2	AAR5241	Rat STX 8
25	346.5	16.5	222	2	AAR5245	Human STX
26	290.5	13.8	273	7	ABR2846	Human car
27	272	12.9	122	4	AAG4710	Human col
28	224	10.7	50	5	ABP4610	Human ORF
29	221	10.5	328	10	AE86158	Human del
30	221	10.5	343	10	AE86090	Human del
31	221	10.5	368	10	AE86157	Human del
32	221	10.5	430	10	AE86156	Human del
33	221	10.5	468	4	AA83855	Amino aci
34	221	10.5	468	10	AE86155	Human del
35	221	10.5	476	10	AE86088	Human del
36	221	10.5	491	10	AE86154	Human del
37	221	10.5	522	4	AA83857	Amino aci
38	221	10.5	528	10	AE86153	Human del
39	221	10.5	565	10	AE86086	Human del
40	221	10.5	600	3	AA83856	Membrane-
41	221	10.5	600	3	AA83856	Human PRO
42	221	10.5	600	4	AA83856	Amino aci
43	221	10.5	600	4	AAU2402	Human PRO
44	221	10.5	600	4	AA83523	Human tra
45	221	10.5	600	4	AA83526	Human PRO

ALIGNMENTS

RESULT 1

ADC73011
ID ADC73011 standard; protein; 398 AA.

AC ADC73011;

DT 01-JAN-2004 (first entry)

DE Murine ST8Sia VI protein.

KW O-glycan alpha2,8-sialyltransferase;

KW beta-galactoside alpha2,6-sialyltransferase; cytotostatic; virucide;
KW antiinflammatory; neuroprotective; cancer metastasis; viral infection;
KW inflammation; nerve tissue; murine; mouse; ST8Sia VI; enzyme.

OS Mus sp.

FN WO2003064655-A1.

PD 07-AUG-2003.

PF 30-JAN-2003; 2003WO-JP000883.

PR 30-JAN-2002; 2002JP-00021159.

24-APR-2002; 2002JP-00122673.

(RIKE) RIKEN KK.

Takashima S, Tsujimoto M, Tsuji S;

WPI; 2003-627613/59.

N-PSDB; ADC73012.

Sugar-chain synthases which are sialyltransferases and encoded genes,
applicable in drugs for inhibiting cancer metastasis, preventing viral
infection, inhibiting inflammation and potentiating nerve tissues.

Claim 2; SEQ ID NO 1; 97pp; Japanese.

The invention relates to a novel O-glycan alpha2,8-sialyltransferase
having a novel substrate specificity and selectivity and a novel beta-
galactoside alpha2,6-sialyltransferase having a novel substrate
specificity and selectivity. The enzymes of the invention demonstrate
cytotostatic, virucide, antiinflammatory and neuroprotective activities and
may be applicable in drugs for inhibiting cancer metastasis, preventing
viral infection, inhibiting inflammation and potentiating nerve tissues.

CC The current sequence is that of the murine ST8Sia VI protein of the
CC invention.
XX
SQ Sequence 398 AA;
Query Match 100.0%; Score 2102; DB 7; Length 398;
Best Local Similarity 100.0%; Pred. No. 2e-200;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRSGGTLFALIGSLMLLLMLCPADAPARSLLMEGSRDTSCTSAALKTLWSPTTP 60
Db 1 MRSGGTLFALIGSLMLLLMLCPADAPARSLLMEGSRDTSCTSAALKTLWSPTTP 60
Qy 61 VPRTRNSTYLDKKTQITEKCKDQYSLNSLNKTRYSDDYLOTTINIORCPWNRQAE 120
Db 61 VPRTRNSTYLDKKTQITEKCKDQYSLNSLNKTRYSDDYLOTTINIORCPWNRQAE 120
Qy 121 EYDNFRKLASCDDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Db 121 EYDNFRKLASCDDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Qy 181 YPNQCAVGVNGGILNLSLCAEIDKSDVFRCNLPPTIGTSASKDVGSKTNLVTNPSII 240
Db 181 YPNQCAVGVNGGILNLSLCAEIDKSDVFRCNLPPTIGTSASKDVGSKTNLVTNPSII 240
Qy 241 TLKYNLKEKKAQPLEDISTYGDFAFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Db 241 TLKYNLKEKKAQPLEDISTYGDFAFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSTIEDTPLSHHY 360
Db 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSTIEDTPLSHHY 360
Qy 361 DNMLPKHGFHQPMPKEYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHQPMPKEYSQMLQHLHMRGILKLOFSKCEA 398
RESULT 2
ADC73013
ID ADC73013 standard; protein; 398 AA.
XX
AC ADC73013;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human ST8Sia VI protein.
XX
KW O-glycan alpha2,8-sialyltransferase;
KW beta-galactoside alpha2,6-sialyltransferase; cytostatic; virucide;
KW antiinflammatory; neuroprotective; cancer metastasis; viral infection;
KW inflammation; nerve tissue; human; ST8Sia VI; enzyme.
XX
OS Homo sapiens.
XX
FN WO2003064655-A1.
XX
PD 07-AUG-2003.
XX
PD 30-JAN-2003; 2003WO-JP00883.
XX
PF WPI; 2003-627613/59.
XX
PR 30-JAN-2002; 2002JP-00021159.
XX
PR 24-APR-2002; 2002JP-00122673.
XX
XX (RIKE) RIKEN KK.
XX
PI Takashima S, Teujimoto M, Teuji S;
XX
DR N-PSDB; ADC73014.
XX
XX Sugar-chain synthases which are sialyltransferases and encoded genes,
XX applicable in drugs for inhibiting cancer metastasis, preventing viral

PT infection, inhibiting inflammation and potentiating nerve tissues.
XX
PS Claim 2; SEQ ID NO 3; 97pp; Japanese.
XX
CC The invention relates to a novel O-glycan alpha2,8-sialyltransferase
CC having a novel substrate specificity and selectivity and a novel beta-
CC galactoside alpha2,6-sialyltransferase having a novel substrate
CC specificity and selectivity. The enzymes of the invention demonstrate
CC cytostatic, virucide, antiinflammatory and neuroprotective activities and
CC may be applicable in drugs for inhibiting cancer metastasis, preventing
CC -viral infection, inhibiting inflammation and potentiating nerve tissues.
CC The current sequence is that of the human ST8Sia VI protein of the
CC invention.
XX
SQ Sequence 398 AA;
Query Match 84.1%; Score 1768; DB 7; Length 398;
Best Local Similarity 82.4%; Pred. No. 4.3e-167;
Matches 328; Conservative 30; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MRSGGTLFALIGSLMLLLMLCPADAPARSLLMEGSRDTSCTSAALKTLWSPTTP 60
Db 1 MRSGGTLFALIGSLMLLLMLCPADAPARSLLMEGSRDTSCTSAALKTLWSPTTP 60
Qy 61 VPRTRNSTYLDKKTQITEKCKDQYSLNSLNKTRYSDDYLOTTINIORCPWNRQAE 120
Db 61 VPRTRNSTYLDKKTQITEKCKDQYSLNSLNKTRYSDDYLOTTINIORCPWNRQAE 120
Qy 121 EYDNFRKLASCDDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Db 121 EYDNFRKLASCDDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Qy 181 YPNQCAVGVNGGILNLSLCAEIDKSDVFRCNLPPTIGTSASKDVGSKTNLVTNPSII 240
Db 181 YPNQCAVGVNGGILNLSLCAEIDKSDVFRCNLPPTIGTSASKDVGSKTNLVTNPSII 240
Qy 241 TLKYNLKEKKAQPLEDISTYGDFAFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Db 241 TLKYNLKEKKAQPLEDISTYGDFAFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSTIEDTPLSHHY 360
Db 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSTIEDTPLSHHY 360
Qy 361 DNMLPKHGFHQPMPKEYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHQPMPKEYSQMLQHLHMRGILKLOFSKCEA 398
RESULT 3
AAG66954
ID AAG66954 standard; protein; 247 AA.
XX
AC AAG66954;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human sialic transferase 27 polypeptide.
XX
KW Human, sialic transferase 27; cancer; cytostatic; immunological disease;
KW human immunodeficiency virus; HIV; infection; inflammatory disease.
XX
OS Homo sapiens.
XX
FN CN1298005-A.
XX
PD 06-JUN-2001.
XX
PF 29-NOV-1999; 99CN-00124142.
XX
PR 29-NOV-1999; 99CN-00124142.
XX
XX (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
PA

XX Mao Y, Xie Y, Qiu M;
PI WPI; 2001-489682/54.
DR N-PSDB; AAH77592.
XX Human sialic transferase 27 as one new kind of polypeptide and
PT polynucleotides encoding this polypeptide.
XX
PS Claim 1; Page 22-23 (disclosure); 29pp; Chinese.
XX The invention relates to a novel polypeptide, human sialic transferase
CC 27, polynucleotides encoding this polypeptide and a DNA recombination
CC process to produce the polypeptide. The polypeptide is useful for
CC treating various diseases, such as malignant tumors, nosohaemia, HIV
CC infection, immunological diseases and inflammatory diseases. The
CC invention also provides an antibody directed against the polypeptide. The
CC present sequence is the polypeptide of the invention
XX
SQ Sequence 247 AA;
Query Match 56.1%; Score 1180; DB 4; Length 247;
Best Local Similarity 88.3%; Pred. No. 1e-108;
Matches 218; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 152 MSYEVESEKGIPIRENIHFHMFVSQPFVDYPYNOCAVVGNGGILNKLSCGAEIDKSDVF 211
Db 1 MSYEVESEKGIPIKNIHFHMFVSQPFVDYPYNOCAVVGNGGILNKLSCGTRIDKSDVF 60
QY 212 RCNLPPTGSAKDVGSKTNLVNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 271
Db 61 RCNLPPTGSAKDVGSKTNLVNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 120
QY 272 SYRANTGISFKYQTLKESKQKLVFFHPRYLRHLAFWRTKGVYAVRLSTGLMIASVA 331
Db 121 SPRANTGTSFKYQTLKESKQKLVFFHPRYLRHLAFWRTKGVYAVRLSTGLMIASVA 180
QY 332 VELCNVLYGFWPFSKTIEDTPLSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKQ 391
Db 181 VELCNVLYGFWPFSKTIEDTIPVSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKQ 240
QY 392 FSKCETA 398
Db 241 FSKCEVA 247
RESULT 4
ADV69201
ID ADV69201 standard; protein; 247 AA.
XX
AC ADV69201;
XX
DT 24-FEB-2005 (first entry)
DE Human cell division regulating protein 27 SEQ ID NO 2.
XX
KW cell division regulating protein 27; cancer; cytostatic; HIV infection;
KW anti-HIV; immune disorder.
XX
OS Homo sapiens.
XX
FN CN1493590-A.
XX
PD 05-MAY-2004.
XX
PF 30-OCT-2002; 2002CN-00137726.
XX
PR 30-OCT-2002; 2002CN-00137726.
XX
PR (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PA Mao Y, Xie Y;
PI

DR WPI: 2004-500615/48.
DR N-PSDB; ADV69200.
XX New polypeptide-human cell disintegrate regulatory protein 27 for
PT treating cancer, human immunodeficiency virus infection, and immunopathy.
XX
PS Claim 1; SEQ ID NO 2; 25pp; Chinese.
XX The invention relates to human cell division regulating protein 27, the
CC polynucleotide encoding it, preparing the polypeptide by DNA recombinant
CC techniques, application of the polypeptide in treating diseases, such as
CC cancer, human immunodeficiency virus (HIV) infection, immunopathy and the
CC antagonist of the polypeptide and its medical action and application of
CC the polynucleotide. The present sequence is that of the human cell
CC division regulating protein 27 of the invention.
XX
SQ Sequence 247 AA;
Query Match 56.1%; Score 1180; DB 8; Length 247;
Best Local Similarity 88.3%; Pred. No. 1e-108;
Matches 218; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 152 MSYEVESEKGIPIRENIHFHMFVSQPFVDYPYNOCAVVGNGGILNKLSCGAEIDKSDVF 211
Db 1 MSYEVESEKGIPIKNIHFHMFVSQPFVDYPYNOCAVVGNGGILNKLSCGTRIDKSDVF 60
QY 212 RCNLPPTGSAKDVGSKTNLVNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 271
Db 61 RCNLPPTGSAKDVGSKTNLVNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 120
QY 272 SYRANTGISFKYQTLKESKQKLVFFHPRYLRHLAFWRTKGVYAVRLSTGLMIASVA 331
Db 121 SPRANTGTSFKYQTLKESKQKLVFFHPRYLRHLAFWRTKGVYAVRLSTGLMIASVA 180
QY 332 VELCNVLYGFWPFSKTIEDTPLSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKQ 391
Db 181 VELCNVLYGFWPFSKTIEDTIPVSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKQ 240
QY 392 FSKCETA 398
Db 241 FSKCEVA 247
RESULT 5
ADE56214
ID ADE56214 standard; protein; 359 AA.
XX
AC ADE56214;
XX
DT 29-JAN-2004 (first entry)
DE Rat Protein BAA08213, SEQ ID NO 2066.
XX
KW Rat; pain; neuronal tissue; gen therapy; spinal segmental nerve injury;
KW chronic constriction injury; CC; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX

DT 26-JUN-1995 (first entry)
 DE Human alpha-2,8-sialyltransferase protein.
 XX Human; alpha-2,8-sialyltransferase; sialyltransferase; melanoma; E.coli;
 KW pUC119; expression vector; pAMOPRC3Sc; PCR; amplify; primer; sugar chain;
 KW physiological; ganglioside.
 XX Homo sapiens.
 XX WO9423020-A1.
 FN 13-OCT-1994.
 PD 28-MAR-1994; 94WO-JP000495.
 PF 29-MAR-1993; 93JP-00069988.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Sasaki K, Kurata K, Hanai N, Nishi T;
 PI WPI; 1994-333182/41.
 DR N-PSDB; AAQ77831.
 XX New alpha-2,8-sialyl transferase - useful for producing physiologically
 PT active sugar chains.
 XX Claim 1; Page 63-66; 102pp; Japanese.
 XX The amino acid sequence of the novel human alpha-2,8-sialyltransferase.
 CC The gene encodes a protein of 356 a.a. The gene (called WPI) was isolated
 CC from the human melanoma cell line WM266-4 and cloned into the E.coli
 CC plasmid pUC119 to create pUC119.WPI. The gene was inserted into the
 CC expression vector pAMOPRC3Sc to produce the plasmid pAMOPRSWPI. The
 CC missing N-terminal 19 a.a. were inserted into this vector by PCR
 CC amplification using the primers AAQ77835-6. Alpha-2,8-sialyltransferase
 CC is useful in the production of physiologically active sugar chains e.g.
 CC in the conversion of ganglioside GM3 to GD3. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX Sequence 356 AA;
 XX
 Query Match 33.3%; Score 700; DB 2; Length 356;
 Best Local Similarity 43.6%; Pred. No. 1.4e-60;
 Matches 130; Conservative 59; Mismatches 107; Indels 2; Gaps 2;
 QY 99 SEDYLOTITNIQRCPMNRQAEYDNFRKLASCDAIQDFVVSQNTPTVGTNNMSYEVES 158
 DB 53 NEKEIVQGVQLQ-QGTAWRRNQTARAFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
 QY 159 KGHIPRENIHFMPFVSQPFVDYPYNOCAVVGNGGILNKSICGAEIDKSDFFVRCNLPLPI 218
 DB 112 LYSFTIDNSTVSLFPQATPF-QPLKCAVVGNGGILKSCGCGRQIDEANFVRCNLPLPL 170
 QY 219 TGSASDVGSKTNLVTNPSIITKYONKEKKAQFLEDISTYGDFAFLLLPAPSYRANTG 278
 DB 171 SSEYTKDVGSKQLVTANPSIIRQFONLLWSRKTFFVDMNKIYNHSHIYMPAFSMKTGTE 230
 QY 279 ISPKVYOTLKESKMRQKVLPHRHLALFWRTKGTAYRLSTGLMIASVAVELCENV 338
 DB 231 PSLRVYITLSDVGANQVTLFANPFLASIGKFKWRSRGIHAKRLSTGLFLVSAALGLCEEV 290
 QY 339 KLYGFWPFSTIEDTPLSHHYDNNLPKGFHQPMPKESYQMLQLMRGILKLPQSKCE 396
 DB 291 AIYGFWPFVSNMHEQPISSHYYDNLVLPFSGFHAMPPEEFLOLWYLHKIGALRMQLDPCE 348
 RESULT 8
 AAB86207
 ID AAB86207 standard; protein; 356 AA.
 XX
 AC AAB86207;

XX 28-AUG-2001 (first entry)
 DE Human GD3 synthase protein.
 XX GD3 synthase; human; inhibitor; ganglioside; neurological disorder;
 KW anti-ischemic; cerebral; neurological; antineurodegeneration;
 KW antitumor activity; veterinary medicine; cerebral ischemia; stroke;
 KW traumatic brain injury; spinal cord injury; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW multiple sclerosis; brain tumor
 XX Homo sapiens.
 XX DE19958684-A1.
 XX 07-JUN-2001.
 PD 06-DEC-1999; 99DE-01058684.
 PF 06-DEC-1999; 99DE-01058684.
 XX (KNOL) KNOLL AG.
 XX Martin-Villalba A, Schenkel J, Kleber S, Testi R;
 PI WPI; 2001-357289/38.
 DR Use of ganglioside GD3 synthase inhibitors for treating neurological
 PT diseases, e.g. cerebral ischemia or neurodegeneration.
 XX Disclosure; Page 10-11; 16pp; German.
 XX This invention describes a novel use of inhibitors (I) of ganglioside GD3
 CC synthase (II) for treatment of neurological disorders and their
 CC associated indications, symptoms and dysfunctions. The products of the
 CC invention have anti-ischemic, cerebral, neurological,
 CC antineurodegeneration and antitumor activity. (I) are used, in human or
 CC veterinary medicine, to treat cerebral ischemia, (acute) stroke,
 CC traumatic brain or spinal cord injuries, and neurodegenerative diseases
 CC (especially Alzheimer's and Parkinson's diseases, amyotrophic lateral
 CC sclerosis and multiple sclerosis), also brain tumors that cause injury to
 CC the brain. This sequence represents the human GD3 synthase described in
 CC the method of the invention
 XX Sequence 356 AA;
 XX
 Query Match 33.2%; Score 697; DB 4; Length 356;
 Best Local Similarity 43.3%; Pred. No. 2.9e-60;
 Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;
 QY 99 SEDYLOTITNIQRCPMNRQAEYDNFRKLASCDAIQDFVVSQNTPTVGTNNMSYEVES 158
 DB 53 NEKEIVQGVQLQ-QGTAWRRNQTARAFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
 QY 159 KGHIPRENIHFMPFVSQPFVDYPYNOCAVVGNGGILNKSICGAEIDKSDFFVRCNLPLPI 218
 DB 112 LYSFTIDNSTVSLFPQATPF-QPLKCAVVGNGGILKSCGCGRQIDEANFVRCNLPLPL 170
 QY 219 TGSASDVGSKTNLVTNPSIITKYONKEKKAQFLEDISTYGDFAFLLLPAPSYRANTG 278
 DB 171 SSEYTKDVGSKQLVTANPSIIRQFONLLWSRKTFFVDMNKIYNHSHIYMPAFSMKTGTE 230
 QY 279 ISPKVYOTLKESKMRQKVLPHRHLALFWRTKGTAYRLSTGLMIASVAVELCENV 338
 DB 231 PSLRVYITLSDVGANQVTLFANPFLASIGKFKWRSRGIHAKRLSTGLFLVSAALGLCEEV 290
 QY 339 KLYGFWPFSTIEDTPLSHHYDNNLPKGFHQPMPKESYQMLQLMRGILKLPQSKCE 396
 DB 291 AIYGFWPFVSNMHEQPISSHYYDNLVLPFSGFHAMPPEEFLOLWYLHKIGALRMQLDPCE 348
 RESULT 9

ADD48076
 ID ADD48076 standard; protein; 380 AA.
 XX AC
 XX ADD48076;
 XX DT 02-DEC-2004 (revised)
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein XP_008782, SEQ ID NO 13773.
 XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.
 XX OS Unidentified.
 XX PN WO2003016475-A2.
 XX XX
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GHEO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; XP_008782.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX PS Example 1; Page; 1017pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 380 AA;

85 QYSLNSLNKTRYSEDDYLOTTIN-----IQRCPP-WNRQAEYDNFRAKLASCCDAIQ 137
 62 QFALKEL-----DPSGVPVINSLTQELQKPSKWTNRTAFLHOROEILQHVDAIK 112
 138 DFVVSQNTTPVGTNMSYEVESEKHI-PIRENI FHMFPVSOPFDVDPYNQCAVVGNGGILN 196
 113 NFLSTKNSVRIGQMMDYSSHAFVFSISNNFSLLPDVSPIMNKHYNICAVVGNSGILT 172
 197 KSLCGAEIDKSDVFRNCNLPPIITSSASKDVGSKTNLVNPSIITLKYNLK--EKKAQF 254
 173 GSQCGQEQIDKSDVFRNCNAP-TEAFQDVGRKTNLTTFNPISILEKYNNLLTIQDRNFF 231
 255 LEDISYTGDAFLLPAPSYRANTEISFKYVQTLKESKMRQKVLFFHP-RVLRHLALFWRT 313
 232 FLSLKKLDGAILWIPAFFHTSAFVTRTLVDFVHRHGQKLQVLAWPGNIMQHVNRVWKN 291
 314 KGVTAVRLSTGLMIASVAVELCEVLYGFWPPS---KTIEDTPLSHHYDDNMLPK---- 366
 292 KHLSPRLSTGILMYTLASAICEIHLHGFWPFGFDNTRDLP--YHYDCKGKTETTK 349
 367 -HGFHQMPEYSQMLQLMRGILKQFSKC 395
 350 WQESHQQLPAEFQLLYRMHGEGLETLTSLSHC 379

RESULT 10
 ADD48074
 ID ADD48074 standard; protein; 380 AA.
 XX AC ADD48074;
 XX DT 02-DEC-2004 (revised)
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein AAB50061, SEQ ID NO 13771.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX OS Unidentified.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GHEO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; AAB50061.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX PS Example 1; Page; 1017pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 380 AA;

XX PD 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-JP004192.
 XX PR 18-MAY-2000; 2000JP-00145977.
 XX PA (UYN1-) UNIV NIHOON SCHOOL JURIDICAL PERSON.
 XX FI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX DR WPI; 2002-034733/04.
 XX DR N-PSDB; ABI99514.
 XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX PS Claim 2; Page 1379-1381; 2690pp; English.
 XX CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in AB57020 to AB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX SQ Sequence 380 AA;
 Query Match 22.4%; Score 470; DB 5; Length 380;
 Best Local Similarity 33.1%; Pred. No. 1.4e-37;
 Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;
 QY 69 YLDEKTTQITEKCKDQVSVSNLTKRYSEDDYLTQITNIORCP--WNRQAEYDNFR 126
 DB 67 FLQDSFVPIT-----NSLTHTHE-----LQKPSKWTNRTAFHLQR 101
 QY 127 AKLASCDDAIQDFVSVSNTPVGTNMSYEVESKKHI-PIRENIHMFPPVSVQFVDYPYQ 185
 DB 102 QEILQHVVDVINKFSLTKSSVRIGQLMHYDYSKHYVFSISNNFRSLLPDVSPIKKRYNV 161
 QY 186 CAVVNGGILNKSICGAEIDKSDVFRCLNLPITGSASKOVGSKTNLVTNPSIITLKYQ 245
 DB 162 CAVVNGSGILTSQCGQEIIDSDFVSRCNFAP-TEAFHKDVGKRTNLTTFNPSILEKYIN 220
 QY 246 NLK--EKAQPLEDISYGDFAILLPAPSYRANTYGISEKVTQLKESQKQKVLFFHP-R 302
 DB 221 NLLTIQDRNNFELSLKXLDGAILIPAFFFTSATVTTLTLDFFVHRGQLKVLQWAPGN 280
 QY 303 YLRHLALFWRKTGYTAVRLSTGLMIASVAVELCNVLYGWPPFS---KTEDTPLSHHY 359
 DB 281 IMQHVNRVKNKHLSPKRLSTGLMYLAIASICEIHLVYGFWPFGPDNTREDLP--YHY 338
 QY 360 YDNNMLPK-----HGFHQMPEKYSQMLQLHMRGILKLQFSKC 395
 DB 339 YDKGKTFTTKQWESHQLPAEFQLLYRMHGGSLTKLTLSHC 379
 RESULT 13
 AAW05300
 ID AAW05300 standard; protein; 381 AA.
 XX AC AAW05300;
 XX

DT 17-FEB-1997 (revised)
 DT 17-DEC-1996 (first entry)
 DE Sia alpha 2,3Gal Beta 1,4GlcNAc alpha 2,8-sialyltransferase.
 KW Sialyltransferase; oligosialic acids; protein; glycoprotein; glycolipid;
 KW sugar; biosynthesis; cancer; metastasis; spermatozoa; inflammation;
 KW nervous tissue.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Peptide 1..16 /note= "Signal peptide"
 FT Protein 17..381 /note= "Mature protein, claim 1"
 FT Domain 18..33 /note= "Putative transmembrane domain"
 FT Modified-site 93 /note= "Potential N-glycosylation site"
 FT Modified-site 113 /note= "Potential N-glycosylation site"
 FT Region 161..205 /label= "Sialyl motif L"
 FT Modified-site 206 /label= "Potential N-glycosylation site"
 FT Region 301..323 /label= "Sialyl motif S"
 XX EP736602-A2.
 XX PD 09-OCT-1996.
 XX 02-APR-1996; 96EP-00105267.
 XX 03-APR-1995; 95JP-00077469.
 XX (RIKA) INST PHYSICAL & CHEM RES
 XX Teuji S, Yoshida Y, Kojima N, Kurosawa N, Hamamoto T;
 DR WPI; 1996-444889/45.
 DR N-PSDB; AAT39663.
 XX New isolated sialyltransferase enzyme - useful for treating e.g.
 FT hereditary diseases, cancer metastasis, inflammatory reactions or nervous
 FT tissues.
 XX Claim 1; Fig 1; 25pp; English.
 XX The sialyltransferase (SST) is useful as an agent for introducing
 CC oligosialic acids such as di-, tri- or tetra-sialic acids into proteins,
 CC glycoproteins or glycolipids. It can be used in the treatment of
 CC hereditary diseases which involve the lack of enzymes needed for the
 CC biosynthesis of specified sugar chains. It can also be used for the
 CC prevention of cancerous metastasis, maturation of sperm, inhibition of
 CC inflammatory reactions or regeneration and reactivation of nervous
 CC tissues. Revised 19-FEB-1997 for inclusion of full length protein
 CC sequence and features table information
 XX SQ Sequence 381 AA;
 Query Match 22.4%; Score 470; DB 2; Length 381;
 Best Local Similarity 33.1%; Pred. No. 1.4e-37;
 Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;
 QY 69 YLDEKTTQITEKCKDQVSVSNLTKRYSEDDYLTQITNIORCP--WNRQAEYDNFR 126
 DB 68 FLQDSFVPIT-----NSLTHTHE-----LQKPSKWTNRTAFHLQR 102
 QY 127 AKLASCDDAIQDFVSVSNTPVGTNMSYEVESKKHI-PIRENIHMFPPVSVQFVDYPYQ 185
 DB 103 QEILQHVVDVINKFSLTKSSVRIGQLMHYDYSKHYVFSISNNFRSLLPDVSPIKKRYNV 162

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 26, 2006, 23:31:05 ; Search time 50 Seconds
(without alignments)
696.744 Million cell updates/sec
Title: US-10-501-930-1
Perfect score: 2102
Sequence: 1 MRSGGTLFALIGSLMLLLLL.....MLQLHWRGILKQFSKCETA 398
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PCUTUS COMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	705	33.5	368	2	US-09-949-016-8001
2	700	33.3	356	2	US-09-949-016-6307
3	697	33.2	356	2	US-08-361-304A-2
4	470	22.4	339	1	US-08-626-994A-3
5	470	22.4	339	2	US-08-957-742-3
6	470	22.4	364	1	US-08-626-994A-1
7	470	22.4	364	2	US-08-957-742-1
8	419.5	20.0	359	1	US-08-503-133A-2
9	419.5	20.0	359	1	US-08-576-775A-2
10	419.5	20.0	359	1	US-08-972-498-2
11	419.5	20.0	359	2	US-08-899-545-2
12	419.5	20.0	429	2	US-09-949-016-10541
13	408.5	19.4	384	2	US-09-949-016-9465
14	389	18.5	375	1	US-08-446-875-8
15	389	18.5	375	1	US-08-102-385G-8
16	352.5	16.8	222	1	US-08-446-875-14
17	221	10.5	600	2	US-09-991-181-347
18	221	10.5	600	2	US-09-980-444-347
19	221	10.5	600	2	US-09-987-333-347
20	221	10.5	600	2	US-09-992-598-347
21	221	10.5	600	2	US-09-989-735-347
22	221	10.5	600	3	US-09-989-726-347
23	221	10.5	600	3	US-09-997-514-347
24	221	10.5	600	3	US-09-989-728-347
25	221	10.5	600	3	US-09-997-349-347
26	221	10.5	600	3	US-09-997-653-347

ALIGNMENTS

RESULT 1

US-09-949-016-8001
; Sequence 8001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,765
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,428
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8001
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8001

Query Match 33.5%; Score 705; DB 2; Length 368;
Best Local Similarity 39.4%; Pct. No. 3.5e-67;
Matches 146; Conservative 64; Mismatches 145; Indels 16; Gaps 6;

QY	26	PADAPARSRLMGSRDTSGLTKLWSPPTVPRTRNSTYLDKTKTQITEKCKDLQ	85
DB	6	PWDAGAMSPCGARRQTSRGAVL--AWK-----FPRTR--LPMGASALCVVLCWLYI	57
QY	86	YSLNSLSNKTFRYSEDDYLQITINIQPCPNWQAEYDNFRKLASCDAIQDFVVSQNN	145
DB	58	FPVYRLPN-----EKEIVQGVLD-QGTAMRNQTAARAFKQMEDCCDPAHLFAMTKNN	110
QY	146	TPVGTNMSYEVESKHIPRENIHMPVSPQFVDYPPNCAVVGNGGILNKSICGAEID	205
DB	111	SPMGKSNWYDGEFLYSFTIDNSTSLFPQATPF-QLEPLKCAVVGNGGILKSCGGRQID	169
QY	206	KSPDFVRCNLPBITGTSASQDVGSNTLVNTPSITILKYONLKEKAQFLEDISTYDGF	265
DB	170	EANFVWRNCNLPUSSEYTKDVGSLSQLVANPSIIRORFNLLWSRKTVDNMMKIYHSY	229
QY	266	LLLPAPSYRANTGISPKVYQTLKESKMRQKVLFFPHRYLRLHALFWRTKGTAYRLSTGL	325
DB	230	IYMPAFSMKTGTSPSLRVYVTLSEVGNQTVLPANPNFLRSIGKFWKSRGHHAKRLSTGL	289

Qy 326 MIASVAVELCNVLYGFWPFSKTIETDPLSHHYDNNLPRKHGHQMPKEYSQMLQLHMR 385
Db 290 FLVSAALGLCEVAIYGFWPFSVNMHEQPISHHYDNNLVLPFGFHAMPEBFLQLWYLHKI 349
Qy 386 GILKLOFSKCE 396
Db 350 GALKRQLDPC 360

RESULT 2

US-09-949-016-6307
; Sequence 6307, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6307
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6307

Query Match 33.3%; Score 700; DB 2; Length 356;

Best Local Similarity 43.6%; Pred. No. 1.2e-66;
Matches 130; Conservative 59; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQTTNIQRCPNRQAEYDNFRKALASCCDAIQDFVVSQNNTPVGTNNMSYEVS 158
Db 53 NEKEIVQGVQLQ-QGTAWRRNQTPAFRQKQMEDCCDPAHLFAMTKMNSPMGKSNWYDGEF 111
Qy 159 KKHIPRENIHFMPVSPQFVDYVYNQCAVGVNGGILNKLSCGAEDKSDVFRCNLPPI 218
Db 112 LYSFTIDNSTYSLFPQATPF-QLPKLCVAVGVNGGILKSGCGRQIDEANFVMRCNLPPL 170
Qy 219 TGSASDVGSKTNLVTNPSIITLKYONLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTG 278
Db 171 SSBYTKDVGSKQLVTANPSIIIRQFQNLWSRKTVDNNKIYNSIYMPAFSMKTGTE 230
Qy 279 ISPKVYOTLKESKMRQKVLFFHPRYLRHLALFWRTKGVTAIRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYVYTLSDVGANQVLPANFNFLASIGKFWKSRGIIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSKTIETDPLSHHYDNNLPRKHGHQMPKEYSQMLQLHMRGILKLOFSKCE 396
Db 291 AIYGFWPFVNMHEQPISHHYDNNLVLPFGFHAMPEBFLQLWYLHKI GALKRQLDPC 348

RESULT 3

US-08-361-304A-2
; Sequence 2, Application US/08361304A
; Patent No. 6596523
; GENERAL INFORMATION:
; APPLICANT: SASAKI, KATSUTOSHI
; APPLICANT: MIURA, KAZUMI
; APPLICANT: HANAI, NOBUO
; APPLICANT: NISHI, TATSUNARI
; TITLE OF INVENTION: -2,8-SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361304A
FILING DATE: 29-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/0495
FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP HEI-5-9988
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 356
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-304A-2

Query Match 33.2%; Score 697; DB 2; Length 356;

Best Local Similarity 43.3%; Pred. No. 2.5e-56;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQTTNIQRCPNRQAEYDNFRKALASCCDAIQDFVVSQNNTPVGTNNMSYEVS 158
Db 53 NEKEIVQGVQLQ-QGTAWRRNQTPAFRQKQMEDCCDPAHLFAMTKMNSPMGKSNWYDGEF 111
Qy 159 KKHIPRENIHFMPVSPQFVDYVYNQCAVGVNGGILNKLSCGAEDKSDVFRCNLPPI 218
Db 112 LYSFTIDNSTYSLFPQATPF-QLPKLCVAVGVNGGILKSGCGRQIDEANFVMRCNLPPL 170
Qy 219 TGSASDVGSKTNLVTNPSIITLKYONLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTG 278
Db 171 SSBYTKDVGSKQLVTANPSIIIRQFQNLWSRKTVDNNKIYNSIYMPAFSMKTGTE 230
Qy 279 ISPKVYOTLKESKMRQKVLFFHPRYLRHLALFWRTKGVTAIRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYVYTLSDVGANQVLPANFNFLASIGKFWKSRGIIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSKTIETDPLSHHYDNNLPRKHGHQMPKEYSQMLQLHMRGILKLOFSKCE 396
Db 291 AIYGFWPFVNMHEQPISHHYDNNLVLPFGFHAMPEBFLQLWYLHKI GALKRQLDPC 348

RESULT 4

US-08-626-994A-3
; Sequence 3, Application US/08626994A
; Patent No. 5798244
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: Sial' 2,3Gal' 1,4GlcNAc ' 2,8-SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia


```

; COUNTRY: U.S.A.
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,994A
; FILING DATE: April 3, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: P14595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; US-08-626-994A-1

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Query Match 22.4%; Score 470; DB 1; Length 364;
Best Local Similarity 33.1%; Pred. No. 8.7e-42;
Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;

QY 69 YLDEKTTQITEKCKDLOYSLSNLSNKRYSDDYLQTIITNIQRCP--WNRQAEYDNFR 126
DB 51 FLDSQFVPII-----NSLTHE-----LQEKPSKWTNRTAFLHQR 85

QY 127 AKLASCCDAIQDFVSNQNTVPVGNMYSVESKKHI-PIRENIFHMPVQPFVDYDYNQ 185
DB 86 QEILQHDVNIKFNLSLKSSVRICQLMHYDSSHKYVFSISNNFRSLDPVSPINMKRYN 145

QY 186 CAVVNGGILNKLSCGAEIDKSLVFCNLPPTIGASKDVGSKTNLVTNPSIITLKQY 245
DB 146 CAVVNGSILTSQCGQEIDKSLVFCNLP-TEAFHKDVGKTNLTTFNPSILEKYIN 204

QY 246 NLK--EKAQFLEDISTYGDALFLLPAPFSYRANTGISFKVYQTLKESKMRQKVLFFHP-R 302
DB 205 NLLTIQDRNFFLSKLLDGAIIWIPAFFHTSATVTRTLVDFFVHRGQLKVLAWPGN 264

QY 303 YLRHLALFWRKGTAYRSLTGLMIASVAVELCENVKLYGFWPFS---KTIEDTPLSHHY 359
DB 265 IMQHVNRVYKMKHLSPKRLSTGLMYTLASAICEIHLHYGFWPFGDPNTRDLP--YHY 322

QY 360 YDNMLPK-----HGFHOMPKEYSOMQLQHMKGILKLOFSKC 395
DB 323 YDKKGKFTTKWQESHQLPAPFQQLYRMHGEGLTKLTLSHC 363

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RESULT 7
US-08-957-742-1
; Sequence 1, Application US/08957742
; Patent No. 6017743
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: Sialyltransferase
; TITLE OF INVENTION: Sialyltransferase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia
; COUNTRY: U.S.A.

```

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; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,742
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,994
; FILING DATE: April 3, 1996
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: P14595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; US-08-957-742-1

Query Match 22.4%; Score 470; DB 2; Length 364;
Best Local Similarity 33.1%; Pred. No. 8.7e-42;
Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;

QY 69 YLDEKTTQITEKCKDLOYSLSNLSNKRYSDDYLQTIITNIQRCP--WNRQAEYDNFR 126
DB 51 FLDSQFVPII-----NSLTHE-----LQEKPSKWTNRTAFLHQR 85

QY 127 AKLASCCDAIQDFVSNQNTVPVGNMYSVESKKHI-PIRENIFHMPVQPFVDYDYNQ 185
DB 86 QEILQHDVNIKFNLSLKSSVRICQLMHYDSSHKYVFSISNNFRSLDPVSPINMKRYN 145

QY 186 CAVVNGGILNKLSCGAEIDKSLVFCNLPPTIGASKDVGSKTNLVTNPSIITLKQY 245
DB 146 CAVVNGSILTSQCGQEIDKSLVFCNLP-TEAFHKDVGKTNLTTFNPSILEKYIN 204

QY 246 NLK--EKAQFLEDISTYGDALFLLPAPFSYRANTGISFKVYQTLKESKMRQKVLFFHP-R 302
DB 205 NLLTIQDRNFFLSKLLDGAIIWIPAFFHTSATVTRTLVDFFVHRGQLKVLAWPGN 264

QY 303 YLRHLALFWRKGTAYRSLTGLMIASVAVELCENVKLYGFWPFS---KTIEDTPLSHHY 359
DB 265 IMQHVNRVYKMKHLSPKRLSTGLMYTLASAICEIHLHYGFWPFGDPNTRDLP--YHY 322

QY 360 YDNMLPK-----HGFHOMPKEYSOMQLQHMKGILKLOFSKC 395
DB 323 YDKKGKFTTKWQESHQLPAPFQQLYRMHGEGLTKLTLSHC 363

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RESULT 8
US-08-503-133A-2
; Sequence 2, Application US/08503133A
; Patent No. 5747326
; GENERAL INFORMATION:
; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases.
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue

```

; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/503.133A
; FILING DATE: 17-JULY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503.133
; FILING DATE: 17-JULY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5747336man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-503-133A-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

QY 37 MEGSREDTSGTSAALKTLWSPPTVPTRNSTYLDKTKTQIT---EKCKDLOYSLSLSN 93
DB 1 MRSIRKRWITICTISLLIFKYTKETARTE-----EHQETQLIGDGLC--LSRSLVNSSD 53
QY 94 KTRYSEDDYLTQITNIQRCFWRQAEYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMS 153
DB 54 KIIRKAGSTIFQ--HSVQ--GWRINSSLVLEIRKNILRFLDAERDVSVVKSFKPGDVIH 109
QY 154 YEVESSKKHIPRENIHFMPVSPQFDVYPNQCAVVGNGIILKSLCGAETDKSDVFVRC 213
DB 110 YVLDERRRLTNIHDLHLSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRC 169
QY 214 NLPITGSASKDVGSKTNLVNPSIITLKYNLKEK--KAQFLEDISTYGDALLLPAP 271
DB 170 NLAPEVVEFAA--DVGTGSDFITMPSVQRAFPGGFNEDSRAKVFHRLSMLNDSVLWIPAF 228
QY 272 SYRANTGISPKVQYQTLKESKMRQKVLFPHPRYLRHLALFWRTKGVTA YRLSTGLMIASVA 331
DB 229 MVKGEKHEVWVNNALILKNKLKVRTAYPSLRLIHAVRGYWLTKNVPKPEPTGLMYTLA 288
QY 332 VELCENKLYGFWPFSKTIEDTPLSHHYDNMLPKHGF-----HOMPKYQSOMQLHMR 385
DB 289 TRFCDEIHLGYFWPPKDLNGKAVKHYDDL--KYRYFSNASPHRMPLEFKTLNVLNHR 346
QY 386 GILKLOQSKC 395
DB 347 GALKLITGKC 356

RESULT 9

US-08-576-775A-2
; Sequence 2, Application US/08576775A
; Patent No. 5849904
; GENERAL INFORMATION:

; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of

; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/576.775A
; FILING DATE: 21-December-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503.133
; FILING DATE: 17-July-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-December-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5849904man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-576-775A-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

QY 37 MEGSREDTSGTSAALKTLWSPPTVPTRNSTYLDKTKTQIT---EKCKDLOYSLSLSN 93
DB 1 MRSIRKRWITICTISLLIFKYTKETARTE-----EHQETQLIGDGLC--LSRSLVNSSD 53
QY 94 KTRYSEDDYLTQITNIQRCFWRQAEYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMS 153
DB 54 KIIRKAGSTIFQ--HSVQ--GWRINSSLVLEIRKNILRFLDAERDVSVVKSFKPGDVIH 109
QY 154 YEVESSKKHIPRENIHFMPVSPQFDVYPNQCAVVGNGIILKSLCGAETDKSDVFVRC 213
DB 110 YVLDERRRLTNIHDLHLSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRC 169
QY 214 NLPITGSASKDVGSKTNLVNPSIITLKYNLKEK--KAQFLEDISTYGDALLLPAP 271
DB 170 NLAPEVVEFAA--DVGTGSDFITMPSVQRAFPGGFNEDSRAKVFHRLSMLNDSVLWIPAF 228
QY 272 SYRANTGISPKVQYQTLKESKMRQKVLFPHPRYLRHLALFWRTKGVTA YRLSTGLMIASVA 331
DB 229 MVKGEKHEVWVNNALILKNKLKVRTAYPSLRLIHAVRGYWLTKNVPKPEPTGLMYTLA 288
QY 332 VELCENKLYGFWPFSKTIEDTPLSHHYDNMLPKHGF-----HOMPKYQSOMQLHMR 385
DB 289 TRFCDEIHLGYFWPPKDLNGKAVKHYDDL--KYRYFSNASPHRMPLEFKTLNVLNHR 346
QY 386 GILKLOQSKC 395
DB 347 GALKLITGKC 356

RESULT 10

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US-08-972-498-2
; Sequence 2, Application US/08972498
; Patent No. 5959078
; GENERAL INFORMATION:
; APPLICANT: Gerady-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,498
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/576,775
; FILING DATE: 21-December-1995
; APPLICATION NUMBER: 08/503,133
; FILING DATE: 17-July-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-December-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5959078man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-972-498-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

Qy 37 MEGSRETSGTSAAKLTMSPTVPFRNSTYLDKTTQIT---EKCKDQYSLNSLN 93
Db 1 MRSIRKRWITCTISLLIFYKTKIARTE-----EHOETQIGDGLC--LSRLVNSSD 53

Qy 94 KTRYSEDDYLQITNIQRCPCWNRQAEEYDNFRKLASCCDAIQDFVVSQNNTPVGTNMS 153
Db 54 KIIRKAGSTIFQ--HSVQ--GWRINSSVLVLEIRKNILRFLDAERDVSVVKSFKPGDVH 109

Qy 154 YEVESSKXHIPRENIHFHMFVSPQFVDYPVYVQCAVVGNGGILNKLSCGAETDKSDFVFC 213
Db 110 YVLDRRRTNLNLSHLLPEVSPMKNRRFKTCVAVGNSGILLDSGGCGKEIDSHNFVIRC 169

Qy 214 NLPPTGSASCKVSGKTNLVTPVPSIITLKYQNLKEK--KAQFLEDISTYGDALLPAP 271
Db 170 NLAPVVEFAA--DVGTKSDFITMPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAF 228

Qy 272 SYRANTGISFVYQTLKESKMRQKVLFPHPRYLRLHAFWRTKGTAYRLSTGLMIASVA 331
Db 229 MVKGEKHVEVWNLILKNKLKVRTAYPSLSRLIHAVRGYWLTKVPIKRPSTGLLMYTLA 288

US-08-972-498-2
; Sequence 2, Application US/08972498
; Patent No. 5959078
; GENERAL INFORMATION:
; APPLICANT: Gerady-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,498
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/576,775
; FILING DATE: 21-December-1995
; APPLICATION NUMBER: 08/503,133
; FILING DATE: 17-July-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-December-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5959078man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-972-498-2

Query Match 20.0%; Score 419.5; DB 2; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

Qy 37 MEGSRETSGTSAAKLTMSPTVPFRNSTYLDKTTQIT---EKCKDQYSLNSLN 93
Db 1 MRSIRKRWITCTISLLIFYKTKIARTE-----EHOETQIGDGLC--LSRLVNSSD 53

Qy 94 KTRYSEDDYLQITNIQRCPCWNRQAEEYDNFRKLASCCDAIQDFVVSQNNTPVGTNMS 153
Db 54 KIIRKAGSTIFQ--HSVQ--GWRINSSVLVLEIRKNILRFLDAERDVSVVKSFKPGDVH 109

Qy 154 YEVESSKXHIPRENIHFHMFVSPQFVDYPVYVQCAVVGNGGILNKLSCGAETDKSDFVFC 213
Db 110 YVLDRRRTNLNLSHLLPEVSPMKNRRFKTCVAVGNSGILLDSGGCGKEIDSHNFVIRC 169

Qy 214 NLPPTGSASCKVSGKTNLVTPVPSIITLKYQNLKEK--KAQFLEDISTYGDALLPAP 271
Db 170 NLAPVVEFAA--DVGTKSDFITMPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAF 228

Qy 272 SYRANTGISFVYQTLKESKMRQKVLFPHPRYLRLHAFWRTKGTAYRLSTGLMIASVA 331
Db 229 MVKGEKHVEVWNLILKNKLKVRTAYPSLSRLIHAVRGYWLTKVPIKRPSTGLLMYTLA 288

US-08-972-498-2
; Sequence 2, Application US/0899545-2
; Patent No. 6020201
; GENERAL INFORMATION:
; APPLICANT: Gerady-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503,133
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6020201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-545-2

Query Match 20.0%; Score 419.5; DB 2; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

Qy 37 MEGSRETSGTSAAKLTMSPTVPFRNSTYLDKTTQIT---EKCKDQYSLNSLN 93
Db 1 MRSIRKRWITCTISLLIFYKTKIARTE-----EHOETQIGDGLC--LSRLVNSSD 53

Qy 94 KTRYSEDDYLQITNIQRCPCWNRQAEEYDNFRKLASCCDAIQDFVVSQNNTPVGTNMS 153
Db 54 KIIRKAGSTIFQ--HSVQ--GWRINSSVLVLEIRKNILRFLDAERDVSVVKSFKPGDVH 109

Qy 154 YEVESSKXHIPRENIHFHMFVSPQFVDYPVYVQCAVVGNGGILNKLSCGAETDKSDFVFC 213
Db 110 YVLDRRRTNLNLSHLLPEVSPMKNRRFKTCVAVGNSGILLDSGGCGKEIDSHNFVIRC 169

Qy 214 NLPPTGSASCKVSGKTNLVTPVPSIITLKYQNLKEK--KAQFLEDISTYGDALLPAP 271
Db 170 NLAPVVEFAA--DVGTKSDFITMPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAF 228
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QY 272 SYRANTGISFKYQYQTLKSKKQKQKLVLFPHPRYLRLHALFWRTKGTAYRLSLGLMIASVA 331
DB 229 MVKGGEKHEVWVNAIILKKNLKVTRVPSLRILHIAVGRYWLTKVPIKRPSTGLLMYTLA 288
QY 332 VELCNVLYGFWPFSKTIEDTPLSHHYDNNMLPKHGF-----HQMPEKYSQMLQLHMR 385
DB 289 TRFCDEIHLGFWPFPKDLNGKAVKHYDDL--KYRFSNAPSRMPLEFKTLNVLNHR 346
QY 386 GILKLQFSKC 395
DB 347 GALKLTGKC 356

RESULT 12
US-09-949-016-10541
; Sequence 10541, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10541
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10541

Query Match 20.0%; Score 419.5; DB 2; Length 429;
Best Local Similarity 28.3%; Pred. No. 3.3e-36;
Matches 116; Conservative 77; Mismatches 180; Indels 37; Gaps 11;
QY 12 GSLMLLLRLMLCPAD-APARSLLMESRE-DTSGTAA-----LKTLS----- 56
DB 28 GSRLQALLAFYRPHRDYLPKTEPLYQEKVRELQGLSRAPKRSIRKRWITICTISLL 87
QY 57 ---PTTPVPRNSTYLDKTTQITEKCKDLOYSLSLSNKTTRYSEDDYLTQITNIQRC 113
DB 88 IFYKTKIARTEE-----HQETQLGDGELSLSRSLVNSDDKIIRKAGSSIFO--HNVE-- 139
QY 114 PWRQAEYDNPRAKLASCCDAIQDFVVSQNTPTVGTNMSYEVSCKHPIRENIFHMP 173
DB 140 GWKINSVLIRKNILPLDARDVSVVKSFKPGDVIHYVDRRTLNISHDLHSLLP 199
QY 174 VSQPFVDYVYNOCAVVGNGILNKLSCGAEIDKSDPFVRCNLPPITGSAKDVGSKTNLV 233
DB 200 EVSPMKNRFFKCAVVGNGILLDECGKEIDSHNFVIRCNLAPVVEFAA-DVGTGSDFI 258
QY 234 TVNPSIITLYQNLEK--KAQFLDEDISTYDAFLLLPAPFSYRANTGISFKYQYQTLKSK 291
DB 259 TNNPSVVOAFGGFNRSDREKFVHRLSMLNDSVLWIPAFMYKGGKHEVWVNAIILKKN 318
QY 292 MEQKLVFPHPRYLRLHALFWRTKGTAYRLSLGLMIASVAVELCNVLYGFWPFSKTIE 351
DB 319 LKVRTAYPSLRILHIAVGRYWLTKVPIKRPSTGLLMYTLATFCDEIHLGFWPFPKDLN 378
QY 352 DTPLSHHYDNNMLPKHGF-----HQMPEKYSQMLQLHMRGILKLOFSKC 395
DB 379 GKAVKHYDDL--KYRFSNAPSRMPLEFKTLNVLNHRGALKTTGKC 426

RESULT 13

US-09-949-016-9465
; Sequence 9465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9465
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9465

Query Match 19.4%; Score 408.5; DB 2; Length 384;
Best Local Similarity 28.6%; Pred. No. 4.2e-35;
Matches 99; Conservative 64; Mismatches 140; Indels 43; Gaps 7;
QY 84 LQYSLNSLSNKTTRYSEDDYLTQITNIQRC-----NNRQAEYD 123
DB 50 IRSVNSLSHKSNR-----AEVINGSSPAVVDNRSNESIKHNIQPASSKWRHNTLSL 103
QY 124 NFRKLASCCDAIQDFVVSQNTPTVGTNMSYEVSCKHPIRENIFHMPVQPFVDYDYP 183
DB 104 RIRKQILKFLDAEKDIDSVLKGTHKPGDIHIFDRDSTMNVSQNIYELLPTSPKKNKHF 163
QY 184 NQCAVVGNGILNKLSCGAEIDKSDPFVRCNLPPITGSAKDVGSKTNLVNPSIITLK 243
DB 164 GTCIAVGNISVLLNSGCCQEIADHSFVIRCNLAPVQEYA-RDVGLKTDLVNPSVIQRA. 222
QY 244 YQNL-----KEGQAQFLDEDISTYDAFLLLPAPFSYRANTGISFKYQYQTLKSKMRQKLV 298
DB 223 FEDLVNATWREKLLQRLHSLN--GSILWIPAFWARGGKERVWVNELILKHVNVRTAY 279
QY 299 FHPRYRLHALFWRTKGTAYRLSLGLMIASVAVELCNVLYGFWPFSKTIEDTPLSHH 358
DB 280 PSLRLLHAVRGYWLTKVHIKRPSTGLLMYTLATFCFKQIYLYGFWPFPDLQONQNPVKYH 339
QY 359 YVDNMLPKHGF-----HQMPEKYSQMLQLHMRGILKLOFSKCETA 398
DB 340 YDLSL--KIGYTSQASPHMPLFKALKSLHEQGALKUTVGQCDGA 383

RESULT 14
US-08-446-875-8
; Sequence 8, Application US/08446875
; Patent No. 5858751
; GENERAL INFORMATION:
; APPLICANT: Paulson, James C.
; APPLICANT: Wen, Xiaohong
; APPLICANT: Livingston, Brian Duane
; APPLICANT: Gillespie, William
; APPLICANT: Kelm, Serge
; APPLICANT: Burlingame, Alma L.
; APPLICANT: Medhihradsky, Katalin
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pons, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA

COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-875-8

Query Match 18.5%; Score 389; DB 1; Length 375;
Best Local Similarity 29.3%; Pred. No. 5.2e-33;
Matches 98; Conservative 58; Mismatches 150; Indels 28; Gaps 7;
QY 87 SLNSLNKTRYSDDYLOITN-----IQ--RCPMNRQAEYDNFRAKLASCCDA 135
DB 47 SLHKSNNRAEVINGSSLPVANSNLSKHSIQPASSKWRHNQTLRLRQKILKFLNA 106
QY 136 IQDFVVSQNNTPVGTNMSYEVESSKHIPRENIFHMFVPSQPFVDYPYNOCVAVNGGIL 195
DB 107 EKNISVLKGLTKPGNIHYIFNRSTNVSQNLVELLPRTSPLKNKHFOQCAIVGNSGVL 166
QY 196 NKSICGAEIDKSDVFRCLNPPITGSAKOVGSKTNLVTNPSIITLKYNL-----KEK 250
DB 167 LNSGCGQEIINTHSFVIRCNLAPVQEYA-RNVGLKTNLVTNPSVIQAFENLVNATWREK 225
QY 251 KAQPLEDISTYGDAPFLLLPAPSVANTGISKVQTLKESKVRQKVLFFHPRYLRLHALF 310
DB 226 LLQRLHGLN---GSILWIPAFMARGGKERVENVNALILKHHVNVRTAYPSLRLHLHVRGY 282
QY 311 WRTKGVNTAYRLSTGLMIASVAVELCENVKLYGFWPFSTKTIEDTPLSHHYDNNMLPKHGF- 369
DB 283 WLTNKHVKRPTTGLLMTATRCNQIYLYGFWPFPLNQNDPVKHYHNSL--KYGYT 340
QY 370 -----HOMPKEYSQMLQHLMRGILKLOFSCETA 398
DB 341 SQASPTMPLEFKALKSLHEQGALKLTVGQCNGA 374

RESULT 15
US-08-102-385G-8
Sequence 8, Application US/08102385G
Patent No. 5962294
GENERAL INFORMATION:
APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Kelm, Sarge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradsky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
IDENTIFICATION AND SYNTHESIS OF SIALYLTRANSFERASES
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, 38th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,669
FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-385G-8

Query Match 18.5%; Score 389; DB 1; Length 375;
Best Local Similarity 29.3%; Pred. No. 5.2e-33;
Matches 98; Conservative 58; Mismatches 150; Indels 28; Gaps 7;
QY 87 SLNSLNKTRYSDDYLOITN-----IQ--RCPMNRQAEYDNFRAKLASCCDA 135
DB 47 SLHKSNNRAEVINGSSLPVANSNLSKHSIQPASSKWRHNQTLRLRQKILKFLNA 106
QY 136 IQDFVVSQNNTPVGTNMSYEVESSKHIPRENIFHMFVPSQPFVDYPYNOCVAVNGGIL 195
DB 107 EKNISVLKGLTKPGNIHYIFNRSTNVSQNLVELLPRTSPLKNKHFOQCAIVGNSGVL 166
QY 196 NKSICGAEIDKSDVFRCLNPPITGSAKOVGSKTNLVTNPSIITLKYNL-----KEK 250
DB 167 LNSGCGQEIINTHSFVIRCNLAPVQEYA-RNVGLKTNLVTNPSVIQAFENLVNATWREK 225
QY 251 KAQPLEDISTYGDAPFLLLPAPSVANTGISKVQTLKESKVRQKVLFFHPRYLRLHALF 310
DB 226 LLQRLHGLN---GSILWIPAFMARGGKERVENVNALILKHHVNVRTAYPSLRLHLHVRGY 282
QY 311 WRTKGVNTAYRLSTGLMIASVAVELCENVKLYGFWPFSTKTIEDTPLSHHYDNNMLPKHGF- 369
DB 283 WLTNKHVKRPTTGLLMTATRCNQIYLYGFWPFPLNQNDPVKHYHNSL--KYGYT 340
QY 370 -----HOMPKEYSQMLQHLMRGILKLOFSCETA 398
DB 341 SQASPTMPLEFKALKSLHEQGALKLTVGQCNGA 374

Search completed: May 26, 2006, 23:32:27
Job time : 52 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:43:01 ; Search time 183 Seconds
(without alignments)
1007.429 Million cell updates/sec

Title: US-10-501-930-1
Perfect score: 2102
Sequence: 1 MRSGGTLFALIGSLMLLLLL.....MLQLMRGILKLOFSKCETA 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /EMC_Celerra_SID3/prodata/2/pubppa/US07_PUBCOMB.pcp.*
2: /EMC_Celerra_SID3/prodata/2/pubppa/US08_PUBCOMB.pcp.*
3: /EMC_Celerra_SID3/prodata/2/pubppa/US09_PUBCOMB.pcp.*
4: /EMC_Celerra_SID3/prodata/2/pubppa/US10A_PUBCOMB.pcp.*
5: /EMC_Celerra_SID3/prodata/2/pubppa/US10B_PUBCOMB.pcp.*
6: /EMC_Celerra_SID3/prodata/2/pubppa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2102	100.0	398	5	US-10-501-930-1	Sequence 1, Appli
2	1768	84.1	398	5	US-10-501-930-3	Sequence 3, Appli
3	697	33.2	356	4	US-10-430-325-2	Sequence 2, Appli
4	697	33.2	356	4	US-10-169-989-1	Sequence 1, Appli
5	272	12.9	122	4	US-10-106-698-5484	Sequence 5484, Ap
6	224	10.7	50	3	US-09-867-550-1960	Sequence 1960, Ap
7	221	10.5	600	3	US-09-989-722-347	Sequence 347, App
8	221	10.5	600	3	US-09-989-723-347	Sequence 347, App
9	221	10.5	600	3	US-09-989-727-347	Sequence 347, App
10	221	10.5	600	3	US-09-989-731-347	Sequence 347, App
11	221	10.5	600	3	US-09-989-732-347	Sequence 347, App
12	221	10.5	600	3	US-09-989-733-347	Sequence 347, App
13	221	10.5	600	3	US-09-991-073-347	Sequence 347, App
14	221	10.5	600	3	US-09-990-442-347	Sequence 347, App
15	221	10.5	600	3	US-09-991-163-347	Sequence 347, App
16	221	10.5	600	3	US-09-993-604-347	Sequence 347, App
17	221	10.5	600	3	US-09-990-456-347	Sequence 347, App
18	221	10.5	600	3	US-09-989-721-347	Sequence 347, App
19	221	10.5	600	3	US-09-982-598-347	Sequence 347, App
20	221	10.5	600	3	US-09-989-233A-347	Sequence 347, App
21	221	10.5	600	3	US-09-989-735-347	Sequence 347, App
22	221	10.5	600	3	US-09-990-444-347	Sequence 347, App
23	221	10.5	600	3	US-09-991-181-347	Sequence 347, App
24	221	10.5	600	3	US-09-989-730-347	Sequence 347, App
25	221	10.5	600	3	US-09-990-436-347	Sequence 347, App
26	221	10.5	600	3	US-09-993-687-347	Sequence 347, App
27	221	10.5	600	3	US-09-989-734-347	Sequence 347, App

28	221	10.5	600	3	US-09-997-653-347	Sequence 347, App
29	221	10.5	600	3	US-09-989-724-347	Sequence 347, App
30	221	10.5	600	3	US-09-989-728-347	Sequence 347, App
31	221	10.5	600	3	US-09-990-441-347	Sequence 347, App
32	221	10.5	600	3	US-09-993-667-347	Sequence 347, App
33	221	10.5	600	3	US-09-997-428-347	Sequence 347, App
34	221	10.5	600	3	US-09-997-666-347	Sequence 347, App
35	221	10.5	600	3	US-09-950-438-347	Sequence 347, App
36	221	10.5	600	3	US-09-990-562-347	Sequence 347, App
37	221	10.5	600	3	US-09-990-711-347	Sequence 347, App
38	221	10.5	600	3	US-09-989-726-347	Sequence 347, App
39	221	10.5	600	3	US-09-998-156-347	Sequence 347, App
40	221	10.5	600	3	US-09-990-437-347	Sequence 347, App
41	221	10.5	600	3	US-09-991-157-347	Sequence 347, App
42	221	10.5	600	3	US-09-997-514-347	Sequence 347, App
43	221	10.5	600	3	US-09-997-573-347	Sequence 347, App
44	221	10.5	600	3	US-09-991-172-347	Sequence 347, App
45	221	10.5	600	3	US-09-990-726-347	Sequence 347, App

ALIGNMENTS

RESULT 1
US-10-501-930-1
; Sequence 1, Application US/10501930
; Publication No. US20060057696A1
; GENERAL INFORMATION:
; APPLICANT: TAKASHIMA, Shou
; APPLICANT: TSUJIMOTO, Masafumi
; TITLE OF INVENTION: GLYCOSYLATING ENZYME
; FILE REFERENCE: P25687
; CURRENT APPLICATION NUMBER: US/10501,930
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: PCT/JP03/00883
; PRIOR FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mouse
US-10-501-930-1

Query Match	100.0%;	Score	2102;	DB	5;	Length	398;
Best Local Similarity	100.0%;	Prod. No.	3.8e-191;				
Matches	398;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL
Db	1	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL	MRSGGTLFALIGSLMLLLLLL
Qy	61	VPRTRNSTYDEKTTQITEKCKL	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI
Db	61	VPRTRNSTYDEKTTQITEKCKL	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI	QYSLNSLSNKTTRYSEDDYLTQITNI
Qy	121	EYDNFRKALASCCDAIQDFVVS	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI
Db	121	EYDNFRKALASCCDAIQDFVVS	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI	QNTPVGTNMSYEVSKEKHIPIRENI
Qy	181	YPNQCAVNGGILINKSLCGAE	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS
Db	181	YPNQCAVNGGILINKSLCGAE	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS	DKSDFFVRCNLPTITGSASKDVGS
Qy	241	TLKYNLKEKKAQPLEDISTYGH	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES
Db	241	TLKYNLKEKKAQPLEDISTYGH	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES	AFLLPAPSYRANTGISFKVYQTLKES
Qy	301	PRYLRLHALFWRTKGVTAIRLS	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK
Db	301	PRYLRLHALFWRTKGVTAIRLS	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK	TELMIASVAVELCENKLYGFWPFSK

Qy 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398

RESULT 2

US-10-501-930-3
; Sequence 3, Application US/10501930
; Publication No. US20060057696A1
; GENERAL INFORMATION:
; APPLICANT: TAKASHIMA, Shou
; APPLICANT: TSUJIMOTO, Masafumi
; APPLICANT: TSUJI, Shuichi
; TITLE OF INVENTION: GLYCOSYLATING ENZYME
; FILE REFERENCE: P25687
; CURRENT APPLICATION NUMBER: US/10/501.930
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: PCT/JP03/00883
; PRIOR FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Human
US-10-501-930-3

Query Match 84.1%; Score 1768; DB 5; Length 398;
Best Local Similarity 82.4%; Pred. No. 2.5e-159;
Matches 328; Conservative 30; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MRSGGTLFALIGSLMLLLMLWCPADAPARSLLMGSGREDTSGTSAALKTLWSPTTP 60
Db 1 MRPGCALLALLASLLMLLLLRLLWCPADAPGRARILVEESREATHGTTPAALTLRSPATA 60
Qy 61 VPRTRNSTYLDKTKTQTEKCDLQYSLNSLSNKTREYSEDDYLQTTNIQRCFWRQAE 120
Db 61 VPRATNSTYLNKSLQTEKCNLQYSGESFNKTKYSENDYLIQITDIQSCFWRQAE 120
Qy 121 EYDNFRKALASCCDAIQDFVVSQNTTVPVTNMSYEVESEKHHIPIRENIHMFVVSQPFVD 180
Db 121 EYANFRKALASCCDAVQNFVVSQNTTVPVTNMSYEVESEKKEIPIKKNIFHMFVVSQPFVD 180
Qy 181 YPNQCAVWNGGILNKLSCGAEIDKSDVFRCMLPPTISASKDVGSKNLVTNPSII 240
Db 181 YPNQCAVWNGGILNKLSCGTEIDKSDVFRCMLPPTTGDVSKDVGSKNLVTNPSII 240
Qy 241 TLKYQNLKKEKAQFLEDISTYGDALFLLPAPSVRANTGSGFKVYQTLKESKMRQKVLFFH 300
Db 241 TLKYGNLKKEKALFLEDIATYGDALFFLPAPSVRANTGSGFKVYTLLEESKARQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGTAYRLSTGLMIASVAVELCENVKLYGFWPFSTKTIEDTPLSHYY 360
Db 301 PKYLKOLALFWRTKGTAYRLSTGLMITSVAVELCKNVKLYGFWPFSTKTIEDIPVSHYY 360
Qy 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398

RESULT 3

US-10-430-325-2
; Sequence 2, Application US/10430325
; Publication No. US20040002138A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, KATSUTOSHI
; MIURA, KAZUMI
; HANAI, TOSUO
; NISHI, TATSUNARI
; TITLE OF INVENTION: '-2,8-SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLENN ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/430.325
FILING DATE: 07-May-2004
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361.304A
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: PCT/JP94/00495
FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP 081-5-69988
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 321955
REFERENCE/DOCKET NUMBER: 249-66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 356
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: WM266-4 cell
CELL TYPE: melanoma
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-430-325-2

Query Match 33.2%; Score 697; DB 4; Length 356;

Best Local Similarity 43.3%; Pred. No. 2.5e-57;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLTQTTNIQRCFWRQAEIDNFRKALASCCDAIQDFVVSQNTTVPVTNMSYEVESE 158
Db 53 NEKEIVQGVQLQGTAWRRNQTFRAFRKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
Qy 159 KGHIPRENIHMFVVSQPFVDYPNQCAVWNGGILNKLSCGAEIDKSDVFRCNLPP 218
Db 112 LYSFTTIDNSTYSLFPQATPF-QLEKKCAVWNGGILKKSQCGRQIDEANFVRCNLPL 170
Qy 219 TGSASKDVSKTNLVTNPSIITLKYQNLKKEKAQFLEDISTYGDALFLLPAPSVRANTG 278
Db 171 SSETTKDVGAKSOLVTANPSIIRFQNLWSKTFVNNKITYNHSYIYNPAPSMKTGTE 230
Qy 279 ISPKVYQTLKESKMRQKVLFFHPRYLRLHALFWRTKGTAYRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYTYLSDVGANQTVLFANERFLRSIGFKWKSRIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSTKTIEDTPLSHYYMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCE 396
Db 291 AIYGFWPFSSVMHEQPISSHYYLVLPFGFHAMPEEFLLQMLYLHKIGALRMQLDPCE 348

RESULT 4

US-10-169-989-1
; Sequence 1, Application US/1016989
; Publication No. US20040092438A1
; GENERAL INFORMATION:
; APPLICANT: Martin-Villalba, Ana

```
; APPLICANT: Schenkel, Johannes
; APPLICANT: Kleber, Susanne
; APPLICANT: Testi, Roberto
; TITLE OF INVENTION: USE OF G33-SYNTHASE-INHIBITORS FOR THE TREATMENT OF
; TITLE OF INVENTION: NEUROPATHOLOGICAL DISORDERS AND PROCESS FOR IDENTIFYING
; TITLE OF INVENTION: G33-SYNTHASE-INHIBITORS
; FILE REFERENCE: M/40289
; CURRENT APPLICATION NUMBER: US/10/169,989
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/EP00/12224
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-989-1

Query Match 33.2%; Score 697; DB 4; Length 356;
Best Local Similarity 43.3%; Pred. No. 2.5e-57;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQITITNIQRCPMNRQAEVDNFRKLAASCCDAIQDFVVSQNTTVPVGTNMSYEYES 158
Db 53 NEKEIVQGVLO-QGTAWERNQTAARAFRQKQMEDCCDPAHLFAMTKQNSPMGKSMWYDGEF 111

Qy 159 KKHPIRENIHMPFVPSOPFDVDPYQCAVGVNGGILNKSLGGABIDKSDFFVRCNLPPI 218
Db 112 LYSFTIDNSTYSLFPQATPF-QLPLKCAVGVNGGILKKSGCGROIDEANFVMRCNLPPL 170

Qy 219 TGSASKDVGSKTNLVNPSIITLKYNLKEKKAQFLEDISTYGDFAILLPAFVSRYANTG 278
Db 171 SSETYKDVGAQSQLVANPSIIRQFQNLWSRKTVDNMKINHSYIYMPAFSMTGTE 230

Qy 279 ISFKVYQTLKESKMRQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMIASVAVELCENV 338
Db 231 PSLRVYITLSDVGANQTVLPANPNELRIGKFWKSRGHIHAKELSTGLFLVSAALGLCEV 290

Qy 339 KLYGFWPFSKTIETDPLSHHYDNNMLPKHGFHQPMPKEYSQMLQHMRLGILKQSKCE 396
Db 291 AIYGFWPFSVNMHEQPISHHYDNNVLPFSGFHAMPEEFQLWYLHKIGALRMQLDPCE 348

RESULT 5
US-10-106-698-5484
; Sequence 5484, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5484
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: MISC FEATURE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5484

Query Match 12.9%; Score 272; DB 4; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.6e-17;
Matches 46; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 310 FWRTKGTAVRLSTGLMIASVAVELCENVKLYGFWPFSKTIETDPLSHHYDNNMLPKHQF 369
Db 28 FWKSRGXHAKELSTGLFLVSALXKLCEVAIYGFWPFVSNMHEQPISHHYDNNVLPFSGF 87

Qy 370 HQMPKEYSQMLQHMRLGILKQSKCE 396
Db 88 HAMPEEFQLWYLHKIGALRMQLDPCE 114

RESULT 6
US-09-867-550-1960
; Sequence 1960, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-3)
; CURRENT APPLICATION NUMBER: US/09867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USN 60/308,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1960
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1960

Query Match 10.7%; Score 224; DB 3; Length 50;
Best Local Similarity 86.0%; Pred. No. 1.7e-13;
Matches 43; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 278 GISFKVYQTLKESKMRQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMI 327
Db 1 GTSFKVYITLSESKARQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMI 50

RESULT 7
US-09-989-722-347
; Sequence 347, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
```

APPLICANT:	Kl javin, Ivar J.	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Napier, Mary A.	PRIOR APPLICATION NUMBER:	60/088742
APPLICANT:	Pan, James	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Paoni, Nicholas P.	PRIOR APPLICATION NUMBER:	60/088800
APPLICANT:	Roy, Margaret Ann	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Stewart, Timothy A.	PRIOR APPLICATION NUMBER:	60/088844
APPLICANT:	Tumas, Daniel	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Watanabe, Colin K.	PRIOR APPLICATION NUMBER:	60/088846
APPLICANT:	Williams, P. Mickey	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Wood, William I.	PRIOR APPLICATION NUMBER:	60/088848
APPLICANT:	Zhang, Zemin	PRIOR FILING DATE:	1998-06-11
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER:	60/088860
TITLE OF INVENTION:	Acids Encoding the Same	PRIOR FILING DATE:	1998-06-11
FILE REFERENCE:	P2730F1C63	PRIOR APPLICATION NUMBER:	60/088862
CURRENT APPLICATION NUMBER:	US/09/989,722	PRIOR FILING DATE:	1998-06-16
CURRENT FILING DATE:	2001-11-19	PRIOR APPLICATION NUMBER:	60/088900
PRIOR APPLICATION NUMBER:	60/049787	PRIOR FILING DATE:	1998-06-11
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RESULT 11

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; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napo Leone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; PRIOR FILING DATE: 2001-11-20
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US-09-991-073-347

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; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

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; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC15

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65	PRIOR APPLICATION NUMBER: 60/091982
66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

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RESULT 14

US-09-990-442-347

Sequence 347, Application US/09990-442

Patent No. US20020132252A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C8

CURRENT APPLICATION NUMBER: US/09990-442

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062290

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065195

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

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PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087105

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

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138 PRIOR FILING DATE: 1998-07-07
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140 PRIOR FILING DATE: 1998-07-07
141 PRIOR APPLICATION NUMBER: 60/092182
142 PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

GenCore version 5.1.8
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	150.5	7.2	435	6	US-10-953-349-20494
8	149	7.1	362	6	US-10-196-749-508
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11	126	6.0	404	6	US-10-953-349-34786
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Sequence 22773, A
Sequence 19700, A
Sequence 19699, A
Sequence 19698, A
Sequence 325, App
Sequence 843, App
Sequence 418, App
Sequence 1, Appl
Sequence 2928, A
Sequence 27921, A
Sequence 27920, A
Sequence 3539, Ap
Sequence 310, App
Sequence 30, Appl
Sequence 35, Appl
Sequence 12, Appl
Sequence 4087, Ap

US-10-953-349-22484
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ALIGNMENTS

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US-10-953-349-22484
; Sequence 22484, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10953349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
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; ORGANISM: Glycine max
US-10-953-349-22484

Query Match 7.7%; Score 162.5; DB 6; Length 252;
Best Local Similarity 26.0%; Pred. No. 4.8e-07;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

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; Sequence 22483, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10953349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22484
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22484

```
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22483
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22483

Query Match          7.7%; Score 162.5; DB 6; Length 396;
Best Local Similarity 26.0%; Pred. No. 9e-07;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

QY 183 YNCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVNPSIITL 242
DB 173 YSSCAVVGNGGILLNRDYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 231
QY 243 KYQNLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302
DB 232 ---CARRGGCFCH---PYGDR---VPVIMVICO-ALHFMDY-TVCNASHKAPLLVTDPR 279
QY 303 Y-----LRHLAL---FWRTKGV-----TAYRLSTGLMIASVAVELCENVKLYG 342
DB 280 FDLVCARIVKYSLKRFVEESGKLEKWEAGHDSLFHYSSGMAQVMLALGICDRVSIFG 339
QY 343 FWPFSTKIEDTPLSHHYDNNMLPKHGFHOMPKES 377
DB 340 FG-----KSTSAKHHYTNOKAEHLHLHDYEAAYA 368
```

```
RESULT 3
US-10-953-349-22482
; Sequence 22482, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22482
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22482

Query Match          7.7%; Score 162.5; DB 6; Length 414;
Best Local Similarity 26.0%; Pred. No. 9.6e-07;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

QY 183 YNCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVNPSIITL 242
DB 191 YSSCAVVGNGGILLNRDYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 249
QY 243 KYQNLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302
DB 250 ---CARRGGCFCH---PYGDR---VPVIMVICO-ALHFMDY-TVCNASHKAPLLVTDPR 297
QY 303 Y-----LRHLAL---FWRTKGV-----TAYRLSTGLMIASVAVELCENVKLYG 342
DB 298 FDLVCARIVKYSLKRFVEESGKLEKWEAGHDSLFHYSSGMAQVMLALGICDRVSIFG 357
QY 343 FWPFSTKIEDTPLSHHYDNNMLPKHGFHOMPKES 377
DB 358 FG-----KSTSAKHHYTNOKAEHLHLHDYEAAYA 386
```

RESULT 4

```
US-10-505-928-321
; Sequence 321, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/368,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 321
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-321
```

```
Query Match          7.6%; Score 159; DB 6; Length 331;
Best Local Similarity 25.6%; Pred. No. 1.4e-06;
Matches 63; Conservative 35; Mismatches 80; Indels 68; Gaps 12;

QY 178 FVDYPYNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVNPS 237
DB 110 FDNIPCKCVVVGNGGVLKNTLKEKIDSVDIIRMNNGPVLGH-BEEVGRRTTFRFLFYP 168
QY 238 SIITLKYQNLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTGISFKYQTLKESKMRQKV- 296
DB 169 ESV-----PSDPIHNPNTVILTAFKPHD-----LRWLLELLMGDKIN 207
QY 297 -----LFFHPRYLRLALF-WRTKGVTAAYRL-----STGLMIA 328
DB 208 TNGFWKKPALNLIYKPYQIRILDFIIRT---RAYELLHPFKVPKQKPKHPTTGIITAI 264
QY 329 SVAVELCENVKLYGF-WPFSTKIEDTPLSHHYDNNMLPKHGFHOMPKESQMLQLH 383
DB 265 TLAFYICHEVHLAGKYNFSDL--KSPL--HYIGNATMSLMNNKQAYHNVTAETAE-----QLF 315
QY 384 MRGILK 389
DB 316 LKDIIE 321
```

```
RESULT 5
US-10-953-349-20496
; Sequence 20496, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20496
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20496
```

```
Query Match          7.2%; Score 150.5; DB 6; Length 394;
Best Local Similarity 25.1%; Pred. No. 9.8e-06;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;

QY 183 YNCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVNPSIITL 242
DB 171 YSSCAVVGNGGILLNRNRYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 229
QY 243 KYQNLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302
```

Db 230 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 277
Qy 303 Y-----LRHAL--FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 278 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFYSSGMQAVILALGICDRVSIFG 337
Qy 343 FWPFSTKTIETPLSHHYDDNMLPKHGFHOMPKEYS 377
Db 338 FGKLASA-----KHHYHTNQKAEHLHLHDYEAEYA 366

RESULT 6
US-10-953-349-20495
; Sequence 20495, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20495
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20495

Query Match 7.2%; Score 150.5; DB 6; Length 419;
Best Local Similarity 25.1%; Pred. No. 1.1e-05;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;
Qy 183 YNCAVVGNGGILNKSLGCAEIKSDFFVRCNLPPIITGSASKDVSGKTNLVTNPSIITL 242
Db 196 YSSCAVVGNSGILLNRNYGSEIDSHVIRLNARVDHFETK-VGKKTISIFMNSNLIHL 254
Qy 243 KYONLKEKKAOFLEDISTYGDALFLLPAPSYRANTGISFKVYQTLKESMRQKVLPFFHPR 302
Db 255 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 302
Qy 303 Y-----LRHAL--FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 303 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFYSSGMQAVILALGICDRVSIFG 362
Qy 343 FWPFSTKTIETPLSHHYDDNMLPKHGFHOMPKEYS 377
Db 363 FGKLASA-----KHHYHTNQKAEHLHLHDYEAEYA 391

RESULT 7
US-10-953-349-20494
; Sequence 20494, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20494
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20494

Query Match 7.2%; Score 150.5; DB 6; Length 435;
Best Local Similarity 25.1%; Pred. No. 1.1e-05;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;

Qy 183 YNCAVVGNGGILNKSLGCAEIKSDFFVRCNLPPIITGSASKDVSGKTNLVTNPSIITL 242
Db 212 YSSCAVVGNSGILLNRNYGSEIDSHVIRLNARVDHFETK-VGKKTISIFMNSNLIHL 270
Qy 243 KYONLKEKKAOFLEDISTYGDALFLLPAPSYRANTGISFKVYQTLKESMRQKVLPFFHPR 302
Db 271 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 318
Qy 303 Y-----LRHAL--FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 319 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFYSSGMQAVILALGICDRVSIFG 378
Qy 343 FWPFSTKTIETPLSHHYDDNMLPKHGFHOMPKEYS 377
Db 379 FGKLASA-----KHHYHTNQKAEHLHLHDYEAEYA 407

RESULT 8
US-10-196-749-508
; Sequence 508, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 10/052545
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059283
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059285
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062280
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063180
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063181
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063485
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 508
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-508

Query Match 7.1%; Score 149; DB 6; Length 362;
Best Local Similarity 21.7%; Pred. No. 1.2e-05;
Matches 73; Conservative 50; Mismatches 107; Indels 106; Gaps 16;
Qy 97 RYSEDDVLTQITNTIQRCPWNRQES-EYD-----NFRAKLASCCDAIQDFVVVSQNTIPVG 149

Db 80 RYSVD-----LLPFVQKAPDSEASKYDPPFGFRKFSKVQTLLELLP----- 123
Qy 150 TMSYEVEKXKHIPRENIHFMPVPSQPFVDYVYNQCAVGVNGGILNKSICGABIDKSD 209
Db 124 -----EHLDPHLKAK-----TCRCVVIGSGGILHGLGHTLNQPDV 162
Qy 210 VFRCNLPITGSASQVGSQVGNLVTNPSIITLKQNLKKAQFLEIDISTYGDFAFLLP 269
Db 163 VIRLNSAPVEG-YSEHVGNKTTIRMTYP-----EGAPLSLEYISNDLFVAV 208
Qy 270 AFSYRANTGISFKVYQTL--KESKMRQKVLFF-----HPRYLRHL----- 307
Db 209 LFK-----SVDENWLQAMVKETLPFWRLFPWQVAKPILOPKHFLINPVIIKETAP 263
Qy 308 -----ALFW-RTKGVTAIRYSTGLMIASVAVELCENVKLYGFNPFPSKTIETDPLSH 357
Db 264 DILQYSEFQSRFGWRGDKNVP---TIGVIAVVLATHLDCVSLAGF-GYDLNQPRTEL-- 316
Qy 358 HYDNDM----LPKHGFFHQPMPKEYSQMLQLHMRGILK 389
Db 317 HYFDSQCAAMNFOTMHNVTETTKFLKLKLVKEGVVK 352

RESULT 9
US-10-953-349-12052
; Sequence 12052, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12052
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (197)..(192)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (229)..(229)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (247)..(247)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (272)..(272)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-12052

Query Match 6.6%; Score 138; DB 6; Length 287;
Best Local Similarity 25.0%; Pred. No. 7.6e-05;
Matches 59; Conservative 36; Mismatches 83; Indels 58; Gaps 10;

Qy 166 ENIFHMPVPSQPFVDYVYNQCAVGVNGGILNKSICGABIDKSDVFRCNLPITGSASKD 225
Db 2 EKLSLVLPETPPYPPRQFGRCAVGVNGGILNKTGNEIDGIEYVIRENGAP-TQNYTDY 60
Qy 226 VGSQTNLVTNPSIITL--KYQNLKKAQFLEIDISTYGDFAFLLPAPFSYRANTGISPKV 283
Db 61 VGRKSTRLNRSASAKALDKVVEDEORKEVLIITKIHDIM----- 102
Qy 284 YQTLKESKMRQKVLFFHPRYLR--ALFW-RTKGVTAIRYSTGLMIASVAVELCENVKLYG 342
Db 103 -----NKMIREVPKPNPVVLMISASFGSAAG-----TGLKALBFALSCDSDVMYG 149
Qy 343 P-----WPFKTIETDPLSHHYDNDMLPKGHQMPKEYSQMLQLHMRGILK 390
Db 150 FTVDPGYKEW--TRYFSESQGH-----TPLHG-----RAYQWME--CLGLIKI 190

RESULT 10
US-10-953-349-34787
; Sequence 34787, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34787
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-34787

Query Match 6.0%; Score 126; DB 6; Length 401;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 60; Conservative 23; Mismatches 82; Indels 80; Gaps 9;
Qy 186 CAVVNGGILNKSICGABIDKSDVFRCNLPITGSASKDVGSQTNLVTNPSII----- 240
Db 170 CAVVNGSGTLGSGRGAQIDAHLVIRLNNARVAGFAA-DVGATTGVSVNSNILLHCAV 228
Qy 241 -----TLKYQNLKKAQFLEI-----STYGDFAFLLP----- 270
Db 229 RSAITAPGCACHPYGRAVPLAMVCPQPAHLDDALICNATATPESPFPPLLVTDAIDALCA 288
Qy 271 -----PSYR---ANTGISFKVYQTLKESKMRQKVLFFHPRYLRHLALFWRTKGVTAIRLS 322
Db 289 RIAYYSMRFRVATG-----QPASNWTTRHDERYFH-----YS 322
Qy 323 TGLMIASVAVELCENVKLYGFW--PFSKTIETDPLSHHYDNDMLPKGHQMPKEYSQML 380
Db 323 SGLQAVVMALGACDEVSVFGFHAGAK-----HHYHTNKKKELDLDHDEAYEQFYR 374
Qy 381 QLHMR 385
Db 375 DLQER 379

RESULT 11
US-10-953-349-34786
; Sequence 34786, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

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; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34786
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)..(172)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-34786

Query Match          6.0%; Score 126; DB 6; Length 404;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 60; Conservative 23; Mismatches 82; Indels 80; Gaps 9

QY 186 CAVVNGGILNKLSCGAEIDKSDFFRCNLPPIITGSASKDVGSKTNLVTVPSTII----- 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 173 CAVVNGSGTLLSGRGAQIDAHDLVIRLNNARVAGFAA-DVGATTGVGFVNILLHCAV 231
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 241 -----TLKYONLKEKKAQFLEDI-----STVGDFAILLPA----- 270
      :      :      :      :      :      :      :      :      :      :
Db 232 RSATTPGCACHPYGRAVPLAMVCQPAHLLDALICNATATPESPFLVLVTDAIDALCA 291
      :      :      :      :      :      :      :      :      :      :

QY 271 -----PSYR---ANTGTSFKYVOTLKESKMKQKVLFFHPHYRLHALFWRTKGVTA RL S 322
      :      :      :      :      :      :      :      :      :      :
Db 292 RIAKYNSMRRFVAATG-----QPSNWRTRHDERYFH-----YS 325
      :      :      :      :      :      :      :      :      :      :

QY 323 TGLMIASVAVELCENVKLGFW--PFSKTIETPLSHHYVYDNMLPKGHQMPKEYSQML 380
      :      :      :      :      :      :      :      :      :      :
Db 326 SGLQAVVMALGACDEVSVFGFGKAPGAK-----HHYHTNQKELDLHDYEAAYQFVR 377
      :      :      :      :      :      :      :      :      :      :

QY 381 QLHWR 385
      |
Db 378 DLOER 382
      |

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RESULT 12
US-10-196-749-206
/ Sequence 206, Application US/10196749
/ Publication No. US20060094864A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P34301C340
/ CURRENT APPLICATION NUMBER: US/10/196,749
/ CURRENT FILING DATE: 2002-07-16
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121

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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063485
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063548
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 206
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-206

Query Match          5.9%   Score 123; DB 6; Length 299;
Best Local Similarity 22.1%; Prob. No. 0.0016;
Matches 51; Conservative 34; Mismatches 76; Indels 70; Gaps 8

QY      184  NCACVAVGNGILNKSLCGAIDISDFVFRCNLPPIITGSASKDVSGKT----- 230
DB              :|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:
72  HQCVIVSSSHLLGTKLGPIEPAECTIRNDAPTGG-YSAADVGNKTTYRVVAHSSVPRV 130

QY      231  -----NLVTVPNSIITUKY---COLKEKKAQFLEDISTYGDAFLLLPAPS----- 272
DB              :|||:|||:|||||:|||||:|||||:|||||:|||||:
131  LRRPOEFVNRTPTETVFIFWGPSPSMQXPGOSLVRVIQRAGLVFPFNMEAYAVSPGRMRQFD 190

QY      273  --YRANTGISFKYYQTLESKMKDKVLFFPHRYLRHLALFWRTKGVTAYRLSTGLMIASV 330
DB              :|||:|||:|||||:|||||:|||||:|||||:|||||:
191  DLRFGTGTG-----KDESK-----SHSW-----LSTGWFTWVI 217

QY      331  AVELCENVKLGYGFWP---FSKTEEDTPLSHHYDNMLPKGHGFHOMPKEYSQ 378
DB              :|||:|||:|||||:|||||:|||||:|||||:|||||:
218  AVELCDHVHYGVNPPNYCSORELQRMPHYYPKGPDCVCVTYIQNEHSR 268

RESULT 13
US-10-196-749-536
; Sequence 536, Application US/10196749
; Publication No. US2006094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: F3430R1C340
; CURRENT APPLICATION NUMBER: US/10196749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052568
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059265
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059268
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063488
; PRIOR FILING DATE: 1997-10-21
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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 536
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-536

Query Match 4.1%; Score 86.5; DB 6; Length 210;
Best Local Similarity 28.6%; Pred. No. 1.4;
Matches 24; Conservative 18; Mismatches 41; Indels 1; Gaps 1;
QY 163 PIRENIFHMPVSPFVDYDYPYNOCAVVGNGGILNKSLSGAEIDKSDVFRCNLPPIITGSA 222
Db 57 PLRTHYGIINVKTEPQLDCDLCAIVNSGQVQKVGNEIDRSSCIWRNNAPTGG-Y 115
QY 223 SKOVGSKTNLVNPSIITLKYN 246
Db 116 EEDVGRMTIRVVSHTSVPLLLKN 139

RESULT 14
US-11-293-697-3338
; Sequence 3338, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3338
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3338

Query Match 4.1%; Score 86; DB 7; Length 146;
Best Local Similarity 30.4%; Pred. No. 0.95;
Matches 31; Conservative 17; Mismatches 46; Indels 8; Gaps 4;
QY 186 CAVVNGGILNKSLSGAEIDKSDVFRCNLPPIITGSAKDVGSKTNLVNPSIITLKYN 245
Db 6 CALVTSSGHLHRSQSGQIDQTECVRMNDAPTRG-YGRDVGNTSLRVIAHSSI---Q 60
QY 246 NLKPKKAQFLEDISTYGDALLPAPSYRANTGISFKVYQTL 287
Db 61 RILNRHDLN--VSQGTVFIFWGPSSYMRDGG-KGQVYNL 99

RESULT 15
US-10-196-749-274
; Sequence 274, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052588
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059268
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059268
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062258
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063124
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063124
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063488
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063540
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 274
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-274

Query Match 4.1%; Score 86; DB 6; Length 544;
Best Local Similarity 20.6%; Pred. No. 5.9;
Matches 59; Conservative 42; Mismatches 83; Indels 102; Gaps 15;
QY 90 SLSNKTTRYSEDYLOTITNIOCPWNRQAEYDNFRAKLA-SCCDAIQDFVVSQNNTP- 147
Db 248 SLSREFLLYSPDN-----KRMARNVLKYERLLAESPNHVVAEAVIQRPNI 294
QY 148 -----VGTN-----MSYEVSXKHI---PIRENIFHMPVSPQFVDY 181
Db 295 LQTRDTYEGLCQTLGSOPTLYQISLYCSYETNSNAYLLQPIRKEVHLEPYIALYXDF 354
QY 182 -----PYNQCAVVGCGGILNKSLSGAEIDKSDVFRCNLPPIITGSAKDV 226
Db 355 VSDSEAKQIRELAEPMLQRSVVAEG---EKQLQVEYRISKAWL-----KD- 397
QY 227 GSKTNLVNPSIITLKYN-----NLKPKKAQFLEDISTYGDALLPAPF- 272
Db 398 -----TVDPKLVTLNHRIAALGLDVRPPYAEYIQ-VVNYGIGGHEPHFDHATSPSS 449
QY 273 --YRANTG---ISFKVYQTLKESMRQKVLFP--FHPRYLRHLALFW 311
Db 450 PLYRMKSGNRVATFMVLYLSVEAGATFIYANLSVPVVRNALFW 495

Search completed: May 26, 2006, 23:46:35
Job time : 17 secs